

LENGTH: 32
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: primer
 US-09-770-693-19

Query Match 55.4% Score 13.6, DB 15, Length 25
 Best Local Similarity 80.0% Pred No 1 (e+04)
 Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0

Db 1
 1 TTTCTTATATAGTCTT 20
 2 TTTCTTATATAGTCTT 20

RESULT 21
 US-09-830-133-10
 Sequence 1: Artificial Sequence
 Publication No: US2002024590A1
 GENERAL INFORMATION:
 APPLICANT: 3M Filtronic, Therese
 APPLICANT: Semlaud, Florian
 TITLE OF INVENTION: Data Transfer With Chemical Modifications
 TITLE OF INVENTION: Method Comprising a Step of Inductoresis
 FILE REFERENCE: 01/03 154
 CURRENT AFFILIATION NUMBER: 2001-03-15
 CURRENT FILING DATE: 2001-03-15
 NUMBER OF SEQ ID NOS: 13
 SOFTWARE: Patent version 2.1
 SEQ ID NO 10
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Data delivery
 OTHER INFORMATION: Data delivery
 US-09-844-479-10

Query Match 54.4% Score 13.6, DB 15, Length 25
 Best Local Similarity 80.0% Pred No 1 (e+04)
 Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0

Db 1
 1 TTTCTTATATAGTCTT 20
 2 TTTCTTATATAGTCTT 20

RESULT 22
 US-10-215-112-4755
 Sequence 4755: Application US/10215112
 Publication No: US2003004255A1
 GENERAL INFORMATION:
 APPLICANT: Michael Mitman
 TITLE OF INVENTION: Methods of Sequencing Analysis of Nucleic
 TITLE OF INVENTION: Pools
 FILE REFERENCE: 1113
 CURRENT AFFILIATION NUMBER: US/10/215,112
 CURRENT FILING DATE: 2002-09-09
 NUMBER OF SEQ ID NOS: 1936
 SOFTWARE: Feature for Windows version 4.1
 SEQ ID NO 4755
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Data delivery
 US-10-215-112-4755

Query Match 54.4% Score 13.6, DB 15, Length 25
 Best Local Similarity 80.0% Pred No 1 (e+04)
 Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0

Query 1 TTTCTTATATAGTCTT 20
 Db 20 TTTCTTATATAGTCTT 1

RESULT 23
 US-10-098-263B-19017
 Sequence 19017: Artificial Sequence
 Publication No: US2003010410A1
 GENERAL INFORMATION:
 APPLICANT: Mitman, Michael
 TITLE OF INVENTION: Human Mitochondrial
 FILE REFERENCE: 3118.1
 CURRENT AFFILIATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2001-01-08
 PRICE AFFILIATION NUMBER: 2001-01-08
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 13106
 SOFTWARE: Mitochondrial File Sequence Listing Generation V 1.1
 SEQ ID NO 19017
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien

Query Match 54.4% Score 13.6, DB 15, Length 25
 Best Local Similarity 80.0% Pred No 1 (e+04)
 Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0

Db 5
 1 TTTCTTATATAGTCTT 24
 2 TTTCTTATATAGTCTT 24

RESULT 24
 US-10-098-263B-19018
 Sequence 19018: Artificial Sequence
 Publication No: US2003010410A1
 GENERAL INFORMATION:
 APPLICANT: Mitman, Michael
 TITLE OF INVENTION: Human Mitochondrial
 FILE REFERENCE: 3118.1
 CURRENT AFFILIATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2001-01-08
 PRICE AFFILIATION NUMBER: 2001-01-08
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 13106
 SOFTWARE: Mitochondrial File Sequence Listing Generation V 1.1
 SEQ ID NO 19018
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien

Query Match 54.4% Score 13.6, DB 15, Length 25
 Best Local Similarity 80.0% Pred No 1 (e+04)
 Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0

Db 5
 1 TTTCTTATATAGTCTT 24
 2 TTTCTTATATAGTCTT 24

RESULT 25
 US-10-098-263B-19017C
 Sequence 19017C: Artificial Sequence
 Publication No: US2003010410A1
 GENERAL INFORMATION:
 APPLICANT: Mitman, Michael
 TITLE OF INVENTION: Human Mitochondrial
 FILE REFERENCE: 3118.1
 CURRENT AFFILIATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2001-01-08

Query Match:	52.8%	Score 13.3	DB 12	Length 20
Best Local Similarity:	83.3%	Pred. No. 2.2e-04		
Matches	15	Conservative	0	Indels 0
				Mismatches 3
Cy	6	TTTATATGCTGCTT	23	
	1	TTTTTTTTTTTTTTTT		
Tb	1	TTTATATGCTGCTT	18	

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RESULT 23
US-09-771-913-20
Sequence 218, Application US-09-771-913-20
Publication No. US2003010415A1
GENERAL INFORMATION:
APPLICANT: Gill-Garrison, Rosalynn D
APPLICANT: Mallin, Christopher J
APPLICANT: Sanchez-Polix, Manuel Y
TITLE OF INVENTION: Computer-assisted means for assessing lifestyle risk
FILE REFERENCE: 000,133
CURRENT APPLICATION NUMBER: 09/771,913
PRIORITY FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 205
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 20
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence
US-09-771-913-20

Query Match      52.8%  Score 13.2; EE 12; Length 25;
Best Local Similarity 93.0%  Pctd. No. 2,204,041;
Matches 10; Conservative 0; Mismatches 15; Indels 0; Gaps 0

CY      2 TTTTTCATAGTGGTGT 19
DB      8 TTTTTCATAGTGGTGT 25

RESULT 30
US-10-008-2618-119830
Sequence 218, Application US-10-008-2618-119830
Publication No. US2003010415A1
GENERAL INFORMATION:
APPLICANT: Mallin, Michael
APPLICANT: Sanchez-Polix, Manuel Y
TITLE OF INVENTION: Human Mitochondrion
FILE REFERENCE: 319,1
CURRENT APPLICATION NUMBER: US/10/008,2618
PRIORITY FILING DATE: 2003-01-09
CURRENT FILING DATE: 2003-03-10
PRIOR FILING DATE: 2001-03-10
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11133
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-008-2618-119830

Query Match      52.8%  Score 13.2; EE 12; Length 25;
Best Local Similarity 93.0%  Pctd. No. 2,204,041;
Matches 10; Conservative 0; Mismatches 15; Indels 0; Gaps 0

CY      2 TTTTTCATAGTGGTGT 19
DB      2 TTTTTCATAGTGGTGT 19

RESULT 31
US-10-008-2618-119830
Sequence 218, Application US-10-008-2618-119830
Publication No. US2003010415A1
GENERAL INFORMATION:
APPLICANT: Mallin, Michael
APPLICANT: Sanchez-Polix, Manuel Y
TITLE OF INVENTION: Human Mitochondrion
FILE REFERENCE: 319,1
CURRENT APPLICATION NUMBER: US/10/008,2618
PRIORITY FILING DATE: 2003-01-09
CURRENT FILING DATE: 2003-03-10
PRIOR FILING DATE: 2001-03-10
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 11133
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-008-2618-119830

Query Match      52.8%  Score 13.2; EE 12; Length 25;
Best Local Similarity 93.0%  Pctd. No. 2,204,041;
Matches 10; Conservative 0; Mismatches 15; Indels 0; Gaps 0

CY      2 TTTTTCATAGTGGTGT 19
DB      2 TTTTTCATAGTGGTGT 19

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CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 09/771,913
PRIOR FILING DATE: 2001-03-10
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 119830
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-008-2618-119830

Query Match      52.8%  Score 13; EE 12; Length 25;
Best Local Similarity 93.0%  Pctd. No. 2,204,041;
Matches 10; Conservative 0; Mismatches 15; Indels 0; Gaps 0

CY      4 TTTTTCATAGTGGTGGT 24
DB      3 TTTTTCATAGTGGTGGT 23

RESULT 32
US-09-876-235-37
Sequence 218, Application US-09-876-235-37
Publication No. US2003010415A1
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W
APPLICANT: Libe, Rinde
TITLE OF INVENTION: Selection of binding using RNA-PROTEIN
FILE REFERENCE: 000,750,005
CURRENT APPLICATION NUMBER: 09/876,235
PRIORITY FILING DATE: 2001-06-06
PRIOR APPLICATION NUMBER: 09/247,130
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-03
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/734,963
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/764,491
PRIOR FILING DATE: EARLIER FILING DATE: 1997-11-06
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/687,009
PRIOR FILING DATE: EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: DNA splint
US-09-876-235-37

Query Match      52.8%  Score 13; EE 12; Length 26;
Best Local Similarity 93.7%  Pctd. No. 2,204,041;
Matches 16; Conservative 0; Mismatches 6; Indels 4; Gaps 0

CY      3 TTTTTCATAGTGGTGGT 24
DB      1 TTTTTCATAGTGGTGGT 22

RESULT 33
US-09-729-674-21870
Sequence 218, Application US-09-729-674-21870
Publication No. US2003010415A1
GENERAL INFORMATION:
APPLICANT: Wozniak, Kenneth
APPLICANT: Wozniak, John M
APPLICANT: Lavalley, Edward R
APPLICANT: Collins-Rieley, Lisa A
APPLICANT: Evans, Cheryl
APPLICANT: Wozniak, David
APPLICANT: Treacy, Maurice
US-09-729-674-21870

Query Match      52.8%  Score 13; EE 12; Length 25;
Best Local Similarity 93.0%  Pctd. No. 2,204,041;
Matches 10; Conservative 0; Mismatches 15; Indels 0; Gaps 0

CY      3 TTTTTCATAGTGGTGGT 24
DB      1 TTTTTCATAGTGGTGGT 22

```


2000

APPLICANT Zhang, Jian
APPLICANT Gu, Yizhong
APPLICANT Wang, Guo-Tong
APPLICANT HONG, GUO-JIAN
APPLICANT HONG, GUO-JIAN

```
FILE REFERENCE: PB0158
: CURRENT APPLICATION NUMBER: US/10/060,895A
: CURRENT FILING DATE: 2002-06-10
: PRIOR APPLICATION NUMBER: PCT/US01/00666
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00667
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00664
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00665
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00668
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00663
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: PCT/US01/00670
: PRIOR FILING DATE: 2001-01-30
: PRIOR APPLICATION NUMBER: US 02/864,761
: PRIOR FILING DATE: 2001-05-23
: PRIOR APPLICATION NUMBER: US 60/315,984
: PRIOR FILING DATE: 2001-08-30
: NUMBER OF SEQ ID NOS: 1682
: SOFTWARE: Amdica Sequence Listing Engine
: SEQ ID NO: 856
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Homo sapiens
US 10-060-895A.856
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Query Match      51.2%; Score 12.8; DB 15; Length 25;
Best local Similarity 87.5%; Pred No 149+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
CY      8 TCTATGCTGCTGTGGT 23
      ||| |||||
Db      10 TCAAGTGTGCTGTGGT 25
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Search completed: July 21, 2003, 18:30:43
Job time : 69.3942 secs



GenCore version 5.1.6
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CM nucleic nucleic search, using sw model

Run on: July 21, 2003, 12:51:47, Search time: 641.467 Seconds

(without alignments)
641.166 Million cell updates/sec

Title: US-09-890-363-6

Perfect score: 25

Sequence: 1 tttcttttctatgtgtgtgtgtga g

Scoring table:

Gap: 10 0, Gapext: 1 0

Search: 16164066 seqs, 80074376 residues

Total number of hits satisfying the search criteria: 45120

Minimum DB seq length: 0

Maximum DB seq length: 35

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database:

EST:

1: em_esth1.*
2: em_esth2.*
3: em_esth3.*
4: em_esth4.*
5: em_esth5.*
6: em_esth6.*
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9: em_esth9.*
10: em_esth10.*
11: em_esth11.*
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26: em_esth26.*
27: em_esth27.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	14.4	57.6	38	17 A2630154
2	14.4	57.6	33	17 A2630154
3	14.2	56.8	31	17 A2630154
4	13.9	55.2	30	17 A2630154
5	13.6	54.4	31	17 A2630154

7	13.6	54.4	33	17 A2630154	A2630154 1M0483M6
8	13.4	53.6	25	9 A1495770	A1495770 1M0483M6
9	13.4	53.6	25	9 A1495770	A1495770 1M0483M6
10	13.4	53.6	34	14 A1419301	A1419301 1M0483M6
11	13.2	52.8	19	17 A2630154	A2630154 1M0483M6
12	13.2	52.8	22	17 A2630154	A2630154 1M0483M6
13	13.2	52.8	34	14 A1419301	A1419301 1M0483M6
14	13.2	52.8	22	17 A2630154	A2630154 1M0483M6
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18	13.2	52.8	22	17 A2630154	A2630154 1M0483M6
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83	11.4	45.6	36	17	AD226348	AD226348	CM226348	AD226348	CM226348
84	11.4	45.6	37	17	AD226349	AD226349	CM226349	AD226349	CM226349
85	11.4	45.6	38	17	AD226350	AD226350	CM226350	AD226350	CM226350
86	11.4	45.6	39	17	AD226351	AD226351	CM226351	AD226351	CM226351
87	11.4	45.6	40	17	AD226352	AD226352	CM226352	AD226352	CM226352
88	11.4	45.6	41	17	AD226353	AD226353	CM226353	AD226353	CM226353
89	11.4	45.6	42	17	AD226354	AD226354	CM226354	AD226354	CM226354
90	11.4	45.6	43	17	AD226355	AD226355	CM226355	AD226355	CM226355
91	11.4	45.6	44	17	AD226356	AD226356	CM226356	AD226356	CM226356
92	11.4	45.6	45	17	AD226357	AD226357	CM226357	AD226357	CM226357
93	11.4	45.6	46	17	AD226358	AD226358	CM226358	AD226358	CM226358
94	11.4	45.6	47	17	AD226359	AD226359	CM226359	AD226359	CM226359
95	11.4	45.6	48	17	AD226360	AD226360	CM226360	AD226360	CM226360
96	11.4	45.6	49	17	AD226361	AD226361	CM226361	AD226361	CM226361
97	11.4	45.6	50	17	AD226362	AD226362	CM226362	AD226362	CM226362
98	11.4	45.6	51	17	AD226363	AD226363	CM226363	AD226363	CM226363
99	11.4	45.6	52	17	AD226364	AD226364	CM226364	AD226364	CM226364
100	11.4	45.6	53	17	AD226365	AD226365	CM226365	AD226365	CM226365
101	11.4	45.6	54	17	AD226366	AD226366	CM226366	AD226366	CM226366
102	11.4	45.6	55	17	AD226367	AD226367	CM226367	AD226367	CM226367
103	11.4	45.6	56	17	AD226368	AD226368	CM226368	AD226368	CM226368
104	11.4	45.6	57	17	AD226369	AD226369	CM226369	AD226369	CM226369
105	11.4	45.6	58	17	AD226370	AD226370	CM226370	AD226370	CM226370
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108	11.4	45.6	61	17	AD226373	AD226373	CM226373	AD226373	CM226373
109	11.4	45.6	62	17	AD226374	AD226374	CM226374	AD226374	CM226374
110	11.4	45.6	63	17	AD226375	AD226375	CM226375	AD226375	CM226375
111	11.4	45.6	64	17	AD226376	AD226376	CM226376	AD226376	CM226376
112	11.4	45.6	65	17	AD226377	AD226377	CM226377	AD226377	CM226377
113	11.4	45.6	66	17	AD226378	AD226378	CM226378	AD226378	CM226378
114	11.4	45.6	67	17	AD226379	AD226379	CM226379	AD226379	CM226379
115	11.4	45.6	68	17	AD226380	AD226380	CM226380	AD226380	CM226380
116	11.4	45.6	69	17	AD226381	AD226381	CM226381	AD226381	CM226381
117	11.4	45.6	70	17	AD226382	AD226382	CM226382	AD226382	CM226382
118	11.4	45.6	71	17	AD226383	AD226383	CM226383	AD226383	CM226383
119	11.4	45.6	72	17	AD226384	AD226384	CM226384	AD226384	CM226384
120	11.4	45.6	73	17	AD226385	AD226385	CM226385	AD226385	CM226385
121	11.4	45.6	74	17	AD226386	AD226386	CM226386	AD226386	CM226386
122	11.4	45.6	75	17	AD226387	AD226387	CM226387	AD226387	CM226387
123	11.4	45.6	76	17	AD226388	AD226388	CM226388	AD226388	CM226388
124	11.4	45.6	77	17	AD226389	AD226389	CM226389	AD226389	CM226389
125	11.4	45.6	78	17	AD226390	AD226390	CM226390	AD226390	CM226390
126	11.4	45.6	79	17	AD226391	AD226391	CM226391	AD226391	CM226391
127	11.4	45.6	80	17	AD226392	AD226392	CM226392	AD226392	CM226392
128	11.4	45.6	81	17	AD226393	AD226393	CM226393	AD226393	CM226393
129	11.4	45.6	82	17	AD226394	AD226394	CM226394	AD226394	CM226394
130	11.4	45.6	83	17	AD226395	AD226395	CM226395	AD226395	CM226395
131	11.4	45.6	84	17	AD226396	AD226396	CM226396	AD226396	CM226396
132	11.4	45.6	85	17	AD226397	AD226397	CM226397	AD226397	CM226397
133	11.4	45.6	86	17	AD226398	AD226398	CM226398	AD226398	CM226398
134	11.4	45.6	87	17	AD226399	AD226399	CM226399	AD226399	CM226399
135	11.4	45.6	88	17	AD226400	AD226400	CM226400	AD226400	CM226400
136	11.4	45.6	89	17	AD226401	AD226401	CM226401	AD226401	CM226401
137	11.4	45.6	90	17	AD226402	AD226402	CM226402	AD226402	CM226402
138	11.4	45.6	91	17	AD226403	AD226403	CM226403	AD226403	CM226403
139	11.4	45.6	92	17	AD226404	AD226404	CM226404	AD226404	CM226404
140	11.4	45.6	93	17	AD226405	AD226405	CM226405	AD226405	CM226405
141	11.4	45.6	94	17	AD226406	AD226406	CM226406	AD226406	CM226406
142	11.4	45.6	95	17	AD226407	AD226407	CM226407	AD226407	CM226407
143	11.4	45.6	96	17	AD226408	AD226408	CM226408	AD226408	CM226408
144	11.4	45.6	97	17	AD226409	AD226409	CM226409	AD226409	CM226409
145	11.4	45.6	98	17	AD226410	AD226410	CM226410	AD226410	CM226410
146	11.4	45.6	99	17	AD226411	AD226411	CM226411	AD226411	CM226411
147	11.4	45.6	100	17	AD226412	AD226412	CM226412	AD226412	CM226412
148	11.4	45.6	101	17	AD226413	AD226413	CM226413	AD226413	CM226413
149	11.4	45.6	102	17	AD226414	AD226414	CM226414	AD226414	CM226414
150	11.4	45.6	103	17	AD226415	AD226415	CM226415	AD226415	CM226415
151	11.4	45.6	104	17	AD226416	AD226416	CM226416	AD226416	CM226416
152	11.4	45.6	105	17	AD226417	AD226417	CM226417	AD226417	CM226417

[illegible]

C 956	9	36.8	31	9	AU265883	AU265883
957	9	36.8	31	10	AA280386	AA280386
958	9	36.8	31	10	AA280386	AA280386
959	9	36.8	31	14	AA280386	AA280386
960	9	36.8	31	14	AA280386	AA280386
961	9	36.8	31	17	AA280386	AA280386
962	9	36.8	31	17	AA280386	AA280386
963	9	36.8	31	17	AA280386	AA280386
964	9	36.8	31	17	AA280386	AA280386
965	9	36.8	31	17	AA280386	AA280386
966	9	36.8	31	17	AA280386	AA280386
967	9	36.8	31	17	AA280386	AA280386
968	9	36.8	31	17	AA280386	AA280386
969	9	36.8	31	17	AA280386	AA280386
970	9	36.8	31	17	AA280386	AA280386
971	9	36.8	31	17	AA280386	AA280386
972	9	36.8	31	17	AA280386	AA280386
973	9	36.8	31	17	AA280386	AA280386
974	9	36.8	31	17	AA280386	AA280386
975	9	36.8	31	17	AA280386	AA280386
976	9	36.8	31	17	AA280386	AA280386
977	9	36.8	31	17	AA280386	AA280386
978	9	36.8	31	17	AA280386	AA280386
979	9	36.8	31	17	AA280386	AA280386
980	9	36.8	31	17	AA280386	AA280386
981	9	36.8	31	17	AA280386	AA280386
982	9	36.8	31	17	AA280386	AA280386
983	9	36.8	31	17	AA280386	AA280386
984	9	36.8	31	17	AA280386	AA280386
985	9	36.8	31	17	AA280386	AA280386
986	9	36.8	31	17	AA280386	AA280386
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991	9	36.8	31	17	AA280386	AA280386
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993	9	36.8	31	17	AA280386	AA280386
994	9	36.8	31	17	AA280386	AA280386
995	9	36.8	31	17	AA280386	AA280386
996	9	36.8	31	17	AA280386	AA280386
997	9	36.8	31	17	AA280386	AA280386
998	9	36.8	31	17	AA280386	AA280386
999	9	36.8	31	17	AA280386	AA280386
1000	9	36.8	31	17	AA280386	AA280386

ALIGNMENTS

RESULT 1	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
LOCUS	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
DEFINITION	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
ACCESSION	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
VERSION	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
KEYWORDS	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
SOURCE	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
ORGANISM	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
REFERENCE	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
AUTHORS	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
TITLE	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
JOURNAL	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp
COMMENT	24 bp	24 bp	24 bp	24 bp	24 bp	24 bp

RESULT 1
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

RESULT 2
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., Ste. 100
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0491 row: B column: 14
Seq primer: CACACACCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 33.
Location/Qualifiers
1. 33

FEATURES
SOURCE
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="MIMC1M0491P14"
/clone_11b="Mouse 10b plasmid U03C1M library"
/sex="Male"
/lab_host="F. Coli strain XL10-Gold, TI-resistant, F-"
/note="Vector pMD42uv. Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adapter oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pMD42 (g14732114/jb/AF129272.1), a copy number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-G-1d (Stratagene) cells
and selected for ampicillin resistance."
BASE COUNT
ORIGIN
0 a 1 c 8 g 24 t

Query Match 57.6%; Score 14.4; DB 17; Length 33;
Best Local Similarity 75.0%; Pred. No. 3.6e+05;
Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 TTTTCTTATGCTGCTGCTGCTG 24
||| ||| ||| ||| ||| ||| |||
9 TTTCTTTGCTCTGCTGCTGCTG 32
Db
RESULT 3
AA969179 31 bp mRNA linear EST 07-JUL-1998
LOCUS OPERA104 st Soares_NFL_T_CPG_51 Homo sapiens cDNA clone
DEFINITION IMAGE1581031 y similar to TP-01564 Q1363 EATPO 164 P1NEP0PACT
AA969179 31 bp mRNA linear EST 07-JUL-1998
VERSION AA969179.1 GI:1144359
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 31)
N1 CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLES National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL Comment: Robert Strausberg, Ph.D.
COMMENT Email: cgaps-rtmail.nih.gov
This clone is available royalty-free through LNLN; contact the
IMAGE Consortium (info@imga.lnl.gov) for further information.
Trace considered overall poor quality

Insert Length: 1058 Std Error: 0.00
Seq primer: 40m13 fwd ET from Amerisham
High quality sequence stop: 1.
Location/Qualifiers
1. 31

FEATURES
SOURCE
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE1581031"
/clone_11b="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pTZ19D Pac (pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NHEK12W, testis NIT, and N101;
N1 CGAP-SCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR amplified cDNAs from pools of 1,000 clones made
from the same 3 libraries. The pools consisted of
1 M A 3 E clones 72498-72499, 72499-72500, 72500-72501,
72498-72501, and 72996-73199. Subtraction by both
Soares and M. Fatima Bonaldo."
BASE COUNT
ORIGIN
2 a 3 9 g 18 t

Query Match 56.8%; Score 14.2; DB 9; Length 31;
Best Local Similarity 84.2%; Pred. No. 4.3e+05;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 TTTCTATGCTGCTGCTGCTG 23
||| ||| ||| ||| ||| ||| |||
2 TATCTATGCTGCTGCTGCTG 20
Db

RESULT 4
AZ649722 30 bp DNA linear EST 14-JUN-2001
LOCUS IMAGE1905R Mouse 10kb plasmid U03C1M library Mus musculus genomic
DEFINITION clone U03C1M051905 R, DNA sequence.
ACCESSION AZ649722
VERSION AZ649722.1 GI:11783488
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 30)
Dunn, D., Aoyagi, A., Barber, M., Pearson, T., Dwyer, B., Hamill, J.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Polity,
M., Pose, M., Pose, P., Stokes, P., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., Ste. 100
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0519 row: D column: 05
Seq primer: CACACACCAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 30.
Location/Qualifiers
1. 30

FEATURES
SOURCE
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U03C1M051905"

Insert Length: 1058 Std Error: 0.00
Seq primer: 40m13 fwd ET from Amerisham
High quality sequence stop: 1.
Location/Qualifiers
1. 31

/clone_1lb="Mouse 10kb plasmid U03C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD22v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passages through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (3'-TTCCTTCTATGCTGCTTGGTGA 17, a copy-number of 1000). The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 19 a 6 c 2 g 3 t
 ORIGIN

Query Match 55.2% Score 13.5, Pz 17, Length 10;
 Best Local Similarity 58.2%, Pz 2, g 6, n 6;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

UY 1 TTCCTTCTATGCTGCT 17
 18 TTCTTTTATGCTGCTT 2

Db 18 TTCTTTTATGCTGCTT 2

RESULT 5
 A077462 31 bp cDNA linear GSS 16 FEB-2001
 LOCUS A077462 31 bp cDNA linear GSS 16 FEB-2001
 DEFINITION Musculus musculus 10kb plasmid U03C1M library Mus musculus genomic clone U03C1M000411 F. DNA sequence
 ACCESSION A077462
 VERSION A077462.1 GI:12900155
 KEYWORDS GSS.
 SOURCE house mouse
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 1 (bases 1 to 31)
 Bun, D., Aoyagi, A., Barber, M., Pearson, T., Duval, E., Hamill, J., Islam, H., Longacre, S., Mahmoud, M., Meenah, E., Pedersen, T., Reilly, M., Rose, M., Rose, P., Stokes, P., Tinney, A., von Niederhausern, A., and Wright, D., Weiss, P.
 Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
 Unpublished (2000)
 CONTACT Robert P. Weiss
 UNIVERSITY OF UTAH Genomic Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2000 P., StG, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Inset Length: 10000 Spd Error: 0.00
 Plate: 0004 Row: 1 column: 11
 Seq primer GGTTCATTAACGACGACGACCT
 Class: plasmid ends
 High quality sequence stop: 35.
 Location/Qualifiers
 1..35
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U03C1M000411"

/clone_1lb="Mouse 10kb plasmid U03C1M library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD22v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passages through a 0.05 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD22 (3'-TTCCTTCTATGCTGCTTGGTGA 17, a copy-number of 1000). The vector was ligated with adaptor complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 17 a 6 c 6 g 6 t
 ORIGIN

Query Match 55.2% Score 13.9, Pz 17, Length 35;
 Best Local Similarity 57.8%, Pz 5, g 7, n 6;
 Matches 12; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

UY 1 TTCCTTCTATGCTGCTTGGTGA 25
 33 TTCTTTTATGCTGCTGCTGA 9

Db 33 TTCTTTTATGCTGCTGCTGA 9

RESULT 6
 A1364767 31 bp mRNA linear EST 07-JAN-1999
 LOCUS A1364767 31 bp mRNA linear EST 07-JAN-1999
 DEFINITION Similar to TR-033563 C33563 ESTD 144 F18010181, data sequenced
 ACCESSION A1364767
 VERSION A1364767.1 GI:4124456
 KEYWORDS EST.
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 31)
 NCI-CCGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 CONTACT Robert Strausberg, Ph.D.
 Email: cgs@rsb.illumina.gov
 Tissue procurement: Christopher Moskalko, M.D., Ph.D., Michael F. Emmert-Buck, M.D., Ph.D.
 cDNA library preparation: Life Technologies, Inc.
 cDNA library arrayed by: Greg Lennon, Ph.D.
 DNA sequencing by: Washington University Genome Sequencing Center
 Clone distributed by: NCI CGAP clone distribution information can be found through the L.M.A.G.E. Consortium/LMNC at:
 www.bio.illinois.gov/bioplatform/image/image.html

FEATURES
 source
 1..31
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:1965123"
 /clone_1lb="NCI CGAP 0723"
 /tissue_type="tumor", 5 pooled (see description)"
 /lab_host="DH10B"

Trace considered overall poor quality
 Seq primer: -40UP from GABCO
 High quality sequence stop: 1.
 Location/Qualifiers

Site 1: benign, low-grade, V-shaped, PMW-SFSPG, Site 2: sarcoma; Site 3: NED; cloned unidirectionally. Primer: Oligo dT Average insert size 135 bp. Tumor types: epithelial-mixed Mullerian tumor, papillary serous, clear cell, spindle cell. All are primary tumors, metastasis positive. Life Technologies catalog #: 11574-013

8 C 2 f 0 t

adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTRT3 vector. Library is normalized, and was constructed by Benic Soares and W. Fatima Bonaldo."

BASE COUNT
ORIGIN

15 a 16 c 0 g 1 t

Query Match 53.6%; Score 13.4; DB 9; Length 34;
Best Local Similarity 73.9%; Pred. No. 7.7e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

DB 27 TTTTTCATGCTACGGGCTGA 5

RESULT 11
AZ808350/c

LOCUS

20001114 Mouse 10kb plasmid library Mus musculus genomic

DEFINITION

ACCESSION

AZ808350.1 GI:12974606

VERSION

1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus.

REFERENCE

1 (bases 1 to 19)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beagrie, T., Duvall, R., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Peilly, M., Rose, M., Rose, P., Stokes, P., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

UNIVERSITY OF UTAH

Genome Center

ADDRESS

Rm. 308, Biomedical Research Bldg., 20 S. 2000 E., SUF, UT

84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0071 row: P column: 14

Seq primer: CAGTACGAAACACGCTATACG

Class: plasmid ends

High quality sequence stop: 19.

Location/Qualifiers

1..19

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="M00071P14"

/clone_1kb="mouse 10kb plasmid library"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F⁺

/note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/shares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (p1473214|p1473213), a copy number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and

BASE COUNT
ORIGIN

12 a 4 c 1 g 2 t

Query Match 52.8%; Score 13.2; DB 17; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.6e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 18 TTTTTCATGCTAGT 1

RESULT 12
AZ806134

LOCUS

20001114 Mouse 10kb plasmid library Mus musculus genomic

DEFINITION

ACCESSION

AZ806134.1 GI:12966945

VERSION

1

KEYWORDS

GSS.

SOURCE

house mouse.

ORGANISM

Mus musculus.

REFERENCE

1 (bases 1 to 22)

AUTHORS

Dunn, D., Aoyagi, A., Barber, M., Beagrie, T., Duvall, R., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pedersen, T., Peilly, M., Rose, M., Rose, P., Stokes, P., Tingey, A., von Niederhausern, A., and Wright, D., Weiss, R.

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss

UNIVERSITY OF UTAH

Genome Center

ADDRESS

Rm. 308, Biomedical Research Bldg., 20 S. 2000 E., SUF, UT

84112, USA

TEL: 801 585 5606

FAX: 801 585 7177

EMAIL: dunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0068 row: D column: 05

Seq primer: CAGTACGAAACACGCTATACG

Class: plasmid ends

High quality sequence stop: 22.

Location/Qualifiers

1..22

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="M00068D05"

/clone_1kb="mouse 10kb plasmid library"

/sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F⁺

/note="Vector: PWD42ny; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource

(http://www.jax.org/resources/documents/shares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (p1473214|p1473213), a copy number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and

purified. The sheared, adapted mouse DNA was annealed to
 purified vector DNA, and transformed into
 chemically competent E. coli XL103. The transformants were
 and selected for ampicillin resistance."

BASE COUNT

0 a 4 c 5 g 13 t

Query Match 52.8% Score 13.2 DB 17 Length 22
 Best Local Similarity 83.3% Pred. No. 9.5e+05
 Matches 15 Conservative 0 Mismatches 1 Indels 0 Gaps 0

2 TTTCTTTCTATGCTGCT 19
 3 TTTCTTTCTATGCTGCT 20

RESULT 13

COL136/c

Accession COL136
 Version COL136
 Keywords EST
 Source Human
 Organism Homo sapiens

Location 34 bp mRNA strand EST 23 Job 1000
 Description COL136
 Sequence COL136
 EST COL136
 EST COL136

Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

1 (bases 1 to 24)
 RefSeq: human gene expression database
 Contact: Okada, K.
 Institute for Molecular and Cellular Biol
 Osaka University
 1-3, Yamadaoka, Suita, Osaka Pref. 565, Japan
 Tel: 06-877-5111 (ex.3315)

Human gene signature, 3'-directed cDNA sequence. We are not
 submitting the same cDNA sequence for similarity. The same
 For the abundance information of clones with this sequence in the
 library and as well as in other 3'-directed libraries, see
 http://www.ncbi.nlm.nih.gov/blast/blast.cgi. The sequence of the clones
 represented by this 3' sequence is also found there.

Features
 Location/Qualifiers
 1..34
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="Human adult (Kikuchi)"
 /dev_stage="adult"

Query Match 52.8% Score 13.2 DB 17 Length 22
 Best Local Similarity 83.3% Pred. No. 9.5e+05
 Matches 15 Conservative 0 Mismatches 1 Indels 0 Gaps 0

2 TTTCTTTCTATGCTGCT 19
 3 TTTCTTTCTATGCTGCT 20

BASE COUNT 22 a 4 c 5 g 13 t
 ORIGIN

Query Match 52.8% Score 13.2 DB 17 Length 22
 Best Local Similarity 83.3% Pred. No. 9.5e+05
 Matches 15 Conservative 0 Mismatches 1 Indels 0 Gaps 0

2 TTTCTTTCTATGCTGCT 19
 3 TTTCTTTCTATGCTGCT 20

BASE COUNT 22 a 4 c 5 g 13 t
 ORIGIN

Query Match 52.8% Score 13.2 DB 17 Length 22
 Best Local Similarity 83.3% Pred. No. 9.5e+05
 Matches 15 Conservative 0 Mismatches 1 Indels 0 Gaps 0

2 TTTCTTTCTATGCTGCT 19
 3 TTTCTTTCTATGCTGCT 20

AA929803

Accession AA929803
 Version AA929803
 Keywords EST
 Source Human
 Organism Homo sapiens

Location 22 bp mRNA strand EST 25 Job 1000
 Description AA929803
 Sequence AA929803
 EST AA929803

Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

1 (bases 1 to 22)
 RefSeq: human gene expression database
 Contact: Robert Strausberg, Ph.D.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

Unpublished (1997)
 Author: Robert Strausberg, Ph.D.
 Email: rstraus@nci.nih.gov
 Project: Human Genome Project (HGP)

Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

1 (bases 1 to 22)
 RefSeq: human gene expression database
 Contact: Robert Strausberg, Ph.D.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

Unpublished (1997)
 Author: Robert Strausberg, Ph.D.
 Email: rstraus@nci.nih.gov
 Project: Human Genome Project (HGP)

Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

1 (bases 1 to 22)
 RefSeq: human gene expression database
 Contact: Robert Strausberg, Ph.D.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

Unpublished (1997)
 Author: Robert Strausberg, Ph.D.
 Email: rstraus@nci.nih.gov
 Project: Human Genome Project (HGP)

Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

1 (bases 1 to 22)
 RefSeq: human gene expression database
 Contact: Robert Strausberg, Ph.D.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

Unpublished (1997)
 Author: Robert Strausberg, Ph.D.
 Email: rstraus@nci.nih.gov
 Project: Human Genome Project (HGP)

Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

1 (bases 1 to 22)
 RefSeq: human gene expression database
 Contact: Robert Strausberg, Ph.D.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

Unpublished (1997)
 Author: Robert Strausberg, Ph.D.
 Email: rstraus@nci.nih.gov
 Project: Human Genome Project (HGP)

Human
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo

1 (bases 1 to 22)
 RefSeq: human gene expression database
 Contact: Robert Strausberg, Ph.D.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

REFERENCE

1. (bases 1 to 25)
NCI CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
This clone is available directly from the NIH, contact the
IMAGE Consortium (info@imga1.nih.gov) for further information.
Trace considered overall poor quality
Seq primer: -40ml3 fwd, RT from Amersham
High quality sequence strip: 1

FEATURES

Location/Qualifiers

1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAG-1425060"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organism pooled; Vector: pTZ19-Tag (Pharmacia) with
a modified polylinker site. Not 1, Site 2, Eco RI,
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung Nbl10W, testis NHT, and B-cell
NCL CGAP GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones with
from the same 3 libraries. The pools consisted of
1. M.A.G.E. clones 29740, 30097, 68263, 68739,
72608-728711, and 72906-73139. Subtraction by Benfro
Soares and M. Fatima Bonaldo."

BASE COUNT

19 a 2 c 2 g 2 t

ORIGIN

Query Match 52.0% Score 13, PB 9, Length 25,
Best Local Similarity 76.0%, Freq No 1, 100%,
Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

21 TTTTCTATGCTGCTGCTG 21
21 TTTTCTATGCTGCTGCTG 4

RESULT 16

AZ442116

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC442116 26 bp. RNA. 11047 GGC 21007 1006
clone IMAGE1425060 E. DNA sequence.
AZ442116
AC442116 1 G 10566123
GSS.
house mouse.
Mus musculus
Euphyra; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Robertson, T., Duvall, P., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pederson, T., Peilly,
M., Rose, M., Rose, P., Stokes, P., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10K
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

JOURNAL

Unpublished (2000)

COMMENT

Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

FEATURES

source

Plasmid: 374 row 1, column: 08
Seq primer: TAATAGAGAAATAGTATGATC
Class: plasmid ends
High quality sequence strip: 36.
Location/Qualifiers
1..26

BASE COUNT

6 a 3 c 6 g 11 t

ORIGIN

Query Match 52.0% Score 13, PB 17, Length 26,
Best Local Similarity 76.0%, Freq No 1, 100%,
Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

25 TTTTCTATGCTGCTGCTG 25
25 TTTTCTATGCTGCTGCTG 26

RESULT 17

AZ596498

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AC442116 26 bp. RNA. 11047 GGC 21007 1006
clone IMAGE1425060 E. DNA sequence.
AZ596498
AC596498 1 G 11738088
GSS.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 26)
Dunn, D., Aoyagi, A., Barber, M., Robertson, T., Duvall, P., Hamill, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenan, E., Pederson, T., Peilly,
M., Rose, M., Rose, P., Stokes, P., Tinney, A., von Niederhausern, A.
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10K
Plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunne@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Wed Jul 23 09:24:59 2003

us-09-890-363-6.max.rst

FEATURES
source
Plate: 0409 row: 1 column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 2a
Location/Qualifiers
1..28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M0499L14"
/clone_1b="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F"
/note="Vector: pMD19(+), purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high salt excess. The adapted RNA was purified and size-selected for a 0.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD19 (911472114) [gb|AF129072.1], a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 52.0%; Score 13; DB 17; Length 28;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 3 TCTTTCTATGCTGCTGTGCT 23
DB 5 TCTTTCTATGCTGCTGTGCT 25

RESULT 18
AZ405113 28 bp DNA linear GSS 03-OCT-2000
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
PM 308, Biomedical Polymers Research Bldg, 20 S 2030 E, SMC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

FEATURES
source
Plate: 0173 row: B column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 28
Location/Qualifiers
1..28
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="U06C1M073P16"
/clone_1b="Mouse 10kb plasmid U06C1M library"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, F"
/note="Vector: pMD19(+), purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high salt excess. The adapted RNA was purified and size-selected for a 0.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD19 (911472114) [gb|AF129072.1], a copy number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
Query Match
Best Local Similarity 51.2%; Score 12.8; DB 17; Length 28;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
OY 2 TCTTTCTATGCTGCTGTGCTG 25
DB 1 TCTTTCTATGCTGCTGTGCTG 24

RESULT 19
AA994607 34 bp RNA linear EST 27-AUG-1998
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Human
Human sapiens
Bukayeva, Metazova; Chublaty; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 34)
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: capts@nsl.nih.gov
CDNA Library Preparation: M. Berto Soares, Ph.D., M. Fatima Bonar-de
Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA sequencing by: Washington University Genome Sequencing Center
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAF clone distribution information can be
found through the I.M.A.G.E. Consortium (<http://imgc.ccr.nih.gov/>)
www-bio.11nl.gov/bcrp/image/image.htm
Trace considered overall poor quality

Db TTTTCTTTGTCGTGGAGATG 22

RESULT 24
D19680/c 25 bp mRNA linear EST 12 DEC 1995

LOCUS M19580.1
M19580 mouse 3'-directed Mus musculus domesticus cDNA clone

ACCESSION
VERSION D19580
KEYWORDS EST

SOURCE
ORGANISM western European house mouse,
Mus musculus domesticus
Eukaryote; Moraxia; Chordata; Craniota; Vertebrata; Eumetazoa;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 25)
Kawano,S., Ohyo,Y., Yoshida,T., Katsuki,M., and Matsubara,K.
Analysis of gene expression in mouse embryogenesis by 3' directed
cDNA sequencing
Submitted (1995)

JOURNAL
COMMENT Genbank Entry # AF047458, Ohyo,Y., Yoshida,T., Katsuki,M., and Matsubara,K.
. Institute for Cellular and Molecular Biology
Osaka University
3-1 Yamada-oka, Suita, Osaka 565, Japan.

FEATURES
SOURCE
1..25
Location/Qualifiers
/organism="Mus musculus domesticus"
/strain="C57BL/6J"
/db_xref="taxon:10092"
/contig="mb16ac"
/clone_lib="Mouse 3'-directed"
/tissue_type="fetal tissue (day 6.5-8.5 of gestation)"
BASE COUNT 18 A 3 C 3 G 1 T
ORIGIN

Query Match 49.6% Score 12.4 FR 14 Length 25,
Best Local Similarity 72.7%, Freq No. 178+6,
Matches 16; conservative 0; Mismatches 6; Indels 0; Caps 0;

QY 1 TTTTCTTTATGTCGTGGAGATG 22
||||| ||||| |||||
Mb 25 TTTTCTTTCTTTTCTTGCG 4

RESULT 25
AA867596/c 28 bp mRNA linear EST 16 MAR 1996

LOCUS AA867596.1
AA867596 rat 3'-untranslated cDNA clone IMAGE1294298.5 similar to TR033563 Q33563 EAIRO 164

DEFINITION RATTNOSTLAST,, mRNA sequence.

ACCESSION
VERSION AA867596.1 GI:2963041
KEYWORDS EST

SOURCE
ORGANISM Mus musculus,
house mouse.
Mus musculus.
Eukaryote; Moraxia; Chordata; Craniota; Vertebrata; Eumetazoa;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 28)
Marra,M., Hillier,L., Alton,M., Bowles,M., Dietrich,N., Dubynin,T.,
Geisel,S., Kuchel,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Stephens,M., Tan,F., Underwood,K., Moore,B.,
Theisinger,R., Wylie,T., Lennon,G., Soares,E., Wilson,R. and
Waterson,R.
The WashU-HMI Mouse PST Project
Unpublished (1995)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1815
Email: mouseest@watson.wustl.edu

[illegible]

at <http://www.sanger.ac.uk/ftp/ncbi/blast/>

FEATURES
source

1.330
/organism="Trypanosoma brucei"
/strain="TPE0927"
/db_xref="taxon:5691"
/clone="119b02"

BASE COUNT
7 a 6 c 7 g 10 t

Query Match 48 88; Score 12.2; DB 13; Length 33;
Best Local Similarity 82 48; Pval No 1 9e+06;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 CTATGCTCTGTGTGA 25
|||||
12 CTATGAGCTGTGTGA 28

RESULT 34
R0046766/c 33 bp mRNA 11p11 FET 07 DEC 2001
LOCUS R0046766
DEFINITION R0046766 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone X0104924 3', mRNA sequence.
ACCESSION R0046766
VERSION R0046766.1 GI:1406013
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 33)
AUTHORS Kitayama, A., Toratsuka, C., Mochii, M., Tan, N., Shin-I, T. and Kishida
Y.

REFERENCE
Expressed genes in X laevis oocyte
replicated (1991)
Contact: Tadashi Shin-I
Center For Genetic Research Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tsunagi@nig.ac.jp
Location/Qualifiers
1..33
/organism="Xenopus laevis"
/db_xref="taxon:8155"
/clone="X0104924"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/note="vector: pBSMT, Site 1 NotI, Site 2, EcoRI, COMAS
were oligonucleotide primed and differentially cloned. Strapping
according to Miyawaki and Fabel library is subcloned
and was constructed by N. Tan and A.M. Tori,
(Wellcome/CRC Institute)"

BASE COUNT
20 a 4 c 5 g 4 t

Query Match 48 88; Score 12.2; DB 13; Length 33;
Best Local Similarity 82 48; Pval No 1 9e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTCTATGCTGTGTGA 25
|||||
32 TTTTCTTTTCTATGCTGTGA 8

RESULT 35
AV834098/c 35 bp mRNA linear EST 09-MAY-2002
LOCUS AV834098

DEFINITION

AV834098 cDNA library: Hordem vulgaris vulgaris vulgaris
vulgaris short germination Hordem vulgaris vulgaris cDNA
clone Baga409, mRNA sequence.
ACCESSION AV834098
VERSION AV834098.1 GI:14526187
KEYWORDS EST.
SOURCE Hordem vulgaris subsp. vulgaris.
ORGANISM Hordem vulgaris subsp. vulgaris.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
Triticeae; Hordem.
1 (bases 1 to 35)

REFERENCE
Barley EST sequencing project in NIG and Okayama Univ
Unpublished (2001)
Contact: Kazuhito Sato
Research Institute for Biorenewables
Okayama University, Barley Germplasm Center
Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Email: kazatos@bi.okayama-u.ac.jp,
URL: <http://www.rib.okayama-u.ac.jp/barley/>
Database: <http://www.sanger.ac.uk/ftp/ncbi/blast/>; Barley.LIN1

FEATURES
source

1..35
/organism="Hordem vulgaris subsp. vulgaris"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
/clone="Baga409"
/clone_lib="OK. Sato unpublished cDNA library: Hordem
vulgaris subsp. vulgaris short germination"
/tissue_type="shoots"
/dev_stage="germination"

BASE COUNT
24 a 3 c 2 g 6 t

Query Match 48 88; Score 12.2; DB 10; Length 33;
Best Local Similarity 82 48; Pval No 1 9e+06;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TTCTTTTCTATGCTGTGTGA 25
|||||
28 TTTTCTTTTCTATGCTGA 4

RESULT 36
AA911173/c 42 bp mRNA linear EST 09 JUN 1998

LOCUS AA911173
DEFINITION AA911173 H1 CGAP K143 Homo sapiens cDNA clone IM491126146 3'
similar to TR-04192 44192 NMH1 LETHYDROGENOMER GENE
sequence.
ACCESSION AA911173
VERSION AA911173.1 GI:3000463
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eulalia; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 22)

REFERENCE
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps@mail.nih.gov
Tissue Procurement: Christopher Mokaluk, M.D., Ph.D., Michael R.
Emmett-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LIN1 at:
www.bio.lnhi.gov/bhrp/image/image.html

JOURNAL
COMMENT

AV834098

Islam, H., Mongare, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly



US-10-(00)-835A 95A
Sequence 95A Application US/7060895A
Publication No. US2003014497A1
GENERAL INFORMATION:
CLASSIFICATION:

```

      PRIOR FILING DATE: 2001-01-30
      PRIOR APPLICATION NUMBER: PCT/US01/05670
      PRIOR FILING DATE: 2001-01-30
      PRIOR APPLICATION NUMBER: US 03/864,761
      PRIOR FILING DATE: 2001-05-23
      PRIOR APPLICATION NUMBER: US 60/315,984
      PRIOR FILING DATE: 2001-08-30
      PRIOR FILING DATE: 2001-1682
      NUMBER OF SEQ ID NOS: 1682
      LISTING ENGINE
      SOFTWARE: Acemica Sequence Listing Engine
      SEQ ID NO: 859
      LENGTH: 25
      TYPE: DNA
      ORGANISM: Homo sapiens
      02-10-0607-acaca-859
      Query Match          45.2%   Score 12.8; DB 15; Length 25; Gap=
      Best Local Similarly 80.2%,   P=1E-04; I=7e1e    0; Gap=
      Matches 15; Conservative
      8 TGTATGCGTGGTG 24
      |||||||
      7 TCACAGTCCTGTGGTG 23

```

```

RESULT 13
US-10-060-995A-860 Application US/10060995A
Sequence 860, Application No. US00030104403A1
Publication No. US00030104403A1
GENERAL INFORMATION:
APPLICANT: 3M CO., MINN
INVENTOR: GARY L. TROPE
TITLE OF INVENTION: HUMAN UDP-GALACTOSE 4-EPIPEPTIDE N ACETYLTRANSFERASE ACTIVITY ASSAYS
FILE REFERENCE: PRO/SR
CURRENT FILING DATE: 2001-06-10/00966
PRIOR APPLICATION NUMBER: PCT/US01/00966
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00964
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00968
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/315,984
PRIOR FILING DATE: 2001-08-30
PRIOR FILING DATE: 2001-1682
NUMBER OF SEQ ID NOS: 1682
SEQUENCE: Acetamida Sequence Listing Engine
SEQ ID NO: 860
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
Query Match: 55.2% Score 13.8; DB 15; Length 25;
      15, Conservative Mismatches 0; Indels 0; Gaps 0;
Matches 15, Similarity 9, Mismatches 2;
      8 TGTATGCTGTGTTT 24
      |||
      6 TCAGAGCTGTGTAIS 22
DB

```

PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006658
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006658
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006658
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 09/864,761
 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/315,994
 PRIOR FILING DATE: 2001-09-19
 NUMBER OF SEQ ID NOS: 1682
 SOFTWARE: Acemica Sequence Listing Engine
 SEQ ID NO: 88
 LENGTH: 17
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-060-895A-88

Query Match 55.2%; Score 13.8; DB 15; Length 17;
 Best Local Similarity 89.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 8 TCTATGCTGCTGCTG 24
 |||||
 1 TCAAGCTGCTGCTG 17

RESULT 8
 US-09-918-156 14/c
 Sequence 14, Application US/09318156
 Publication No. US20030104403A1
 GENERAL INFORMATION:
 APPLICANT: Hanany, Francis
 APPLICANT: Lubin, Matthew
 TITLE OF INVENTION: DETECTION OF MUTATED AND SEQUENCE DIFFERENCES USING
 TITLE OF INVENTION: DETECTION OF MUTATED AND SEQUENCE DIFFERENCES
 FILE REFERENCE: 19603/441
 CURRENT FILING DATE: 2001-07-29
 PRIOR APPLICATION NUMBER: US 60/245,136
 PRIOR FILING DATE: 2001-01-30
 NUMBER OF SEQ ID NOS: 76
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 34
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence
 US-09-918-156 14

Query Match 55.2%; Score 13.8; DB 12; Length 21;
 Best Local Similarity 89.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 CY 2 TCTTTTCTATGCTG 18
 |||||
 DB 18 TCTTTTCTATGCTG 2

RESULT 9
 US-09-918-156 14/c
 Sequence 16, Application US/0918156
 Publication No. US20030104403A1
 GENERAL INFORMATION:
 APPLICANT: Hanany, Francis
 APPLICANT: Lubin, Matthew
 TITLE OF INVENTION: DETECTION OF MUTATED AND SEQUENCE DIFFERENCES USING
 TITLE OF INVENTION: DETECTION OF MUTATED AND SEQUENCE DIFFERENCES
 FILE REFERENCE: 19603/441
 CURRENT APPLICATION NUMBER: US/0918156

CURRENT FILING DATE: 2001-07-29
 PRIOR APPLICATION NUMBER: 60/918,156
 PRIOR FILING DATE: 2001-01-30
 NUMBER OF SEQ ID NOS: 76
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 36
 LENGTH: 21
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence
 US-09-918-156 36

Query Match 55.2%; Score 13.8; DB 12; Length 21;
 Best Local Similarity 88.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 2 TCTTTTCTATGCTG 18
 |||||
 DB 18 TCTTTTCTATGCTG 2

RESULT 10
 US-10-060-895A-857
 Sequence 857, Application US/10060895A
 Publication No. US20030104403A1
 GENERAL INFORMATION:
 APPLICANT: Zhang, Jian
 APPLICANT: Gu, Yizhong
 TITLE OF INVENTION: HUMAN CDR3 SALVAGE POLYMERIZATION IN A CELLULAR ENVIRONMENT
 FILE REFERENCE: PB0158
 CURRENT APPLICATION NUMBER: US/10/060,895A
 CURRENT FILING DATE: 2002-06-10
 PRIOR APPLICATION NUMBER: PCT/US01/006667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/006670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/864,761
 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/315,984
 PRIOR FILING DATE: 2001-08-30
 NUMBER OF SEQ ID NOS: 1602
 SOFTWARE: Acemica Sequence Listing Engine
 SEQ ID NO: 857
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-060-895A-857

Query Match 55.2%; Score 13.8; DB 15; Length 25;
 Best Local Similarity 89.2%; Pred. No. 1.3e+04;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 8 TCTATGCTGCTGCTG 24
 |||||
 DB 8 TCAAGCTGCTGCTGCTG 25

RESULT 11

966 10.4 41.6 25 15 US-10-098-2638-21191
 967 10.4 41.6 25 15 US-10-098-2638-22226
 968 10.4 41.6 25 15 US-10-098-2638-24650
 969 10.4 41.6 25 15 US-10-098-2638-27071
 970 10.4 41.6 25 15 US-10-098-2638-29497
 971 10.4 41.6 25 15 US-10-098-2638-31932
 972 10.4 41.6 25 15 US-10-098-2638-34367
 973 10.4 41.6 25 15 US-10-098-2638-36802
 974 10.4 41.6 25 15 US-10-098-2638-39228
 975 10.4 41.6 25 15 US-10-098-2638-41654
 976 10.4 41.6 25 15 US-10-098-2638-44089
 977 10.4 41.6 25 15 US-10-098-2638-46516
 978 10.4 41.6 25 15 US-10-098-2638-48942
 979 10.4 41.6 25 15 US-10-098-2638-51368
 980 10.4 41.6 25 15 US-10-098-2638-53794
 981 10.4 41.6 25 15 US-10-098-2638-56220
 982 10.4 41.6 25 15 US-10-098-2638-58646
 983 10.4 41.6 25 15 US-10-098-2638-61072
 984 10.4 41.6 25 15 US-10-098-2638-63498
 985 10.4 41.6 25 15 US-10-098-2638-65924
 986 10.4 41.6 25 15 US-10-098-2638-68350
 987 10.4 41.6 25 15 US-10-098-2638-70776
 988 10.4 41.6 25 15 US-10-098-2638-73202
 989 10.4 41.6 25 15 US-10-098-2638-75628
 990 10.4 41.6 25 15 US-10-098-2638-78054
 991 10.4 41.6 25 15 US-10-098-2638-80480
 992 10.4 41.6 25 15 US-10-098-2638-82906
 993 10.4 41.6 25 15 US-10-098-2638-85332
 994 10.4 41.6 25 15 US-10-098-2638-87758
 995 10.4 41.6 25 15 US-10-098-2638-90184
 996 10.4 41.6 25 15 US-10-098-2638-92610
 997 10.4 41.6 25 15 US-10-098-2638-95036
 998 10.4 41.6 25 15 US-10-098-2638-97462
 999 10.4 41.6 25 15 US-10-098-2638-99888
 1000 10.4 41.6 25 15 US-10-098-2638-102314

ALIGNMENTS

RESULT 1
 US-10-098-2638-7164

/ Sequence 7164, Application US/100982638
 / Publication No. US2002032119A1
 / GENERAL INFORMATION:
 / APPLICANT: Millman, Michael
 / TITLE OF INVENTION: HUMAN MICRORNA
 / FILE REFERENCE: 3118.1
 / CURRENT APPLICATION NUMBER: US/10/098-2638
 / CURRENT FILING DATE: 2003-01-09
 / PRIORITY APPLICATION NUMBER: 60/220,759
 / PRIORITY FILING DATE: 2001-03-16
 / NUMBER OF SEQ ID NOS: 131066
 / SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 / SEQ ID NO 7164
 / LENGTH: 25
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-10-098-2638-7164

Query Match 56.8%, Score 14.2, DB 10, Length 31,
 Best Local Similarity 81.8%, Freq. No. 2.4e+03,
 Matches 18, Conservative 0, Mismatches 4, Indels 0, Gaps 0

QY 2 TTTTATATGCTGCTGCTGCT 23
 TB 4 TTTTATATGCTGCTGCTGCT 25

RESULT 2
 US-10-098-2638-7164
 / Sequence 7164, Application US/100982638
 / Publication No. US2002032119A1
 / GENERAL INFORMATION:
 / APPLICANT: Millman, Michael
 / TITLE OF INVENTION: HUMAN MICRORNA
 / FILE REFERENCE: 3118.1

/ GENERAL INFORMATION:
 / APPLICANT: EDELMAN, IENA
 / APPLICANT: JACOBSON, ETIENNE DANIEL FRANCOIS
 / APPLICANT: BRIAND, JEAN-PAUL
 / TITLE OF INVENTION: HEMATOPOIETIC MOLECULES CONTAINING A WRITING ARMS TO TARGET
 / TITLE OF INVENTION: SPECIFIC CELLS AND A MOLECULE REGULATING THE APPOPTOSIS
 / TITLE OF INVENTION: PROTEIN OF THE PERMEABILITY TRANSPORT FROM COMPLEX
 / TITLE OF INVENTION: (PPTP)
 / FILE REFERENCE: 01445,0216
 / CURRENT APPLICATION NUMBER: US/10/098-2638-7164
 / CURRENT FILING DATE: 2003-01-09
 / PRIORITY APPLICATION NUMBER: 60/220,759
 / PRIORITY FILING DATE: 2001-03-16
 / NUMBER OF SEQ ID NOS: 135
 / SOFTWARE: Patent in War 2.1
 / SEQ ID NO 260
 / LENGTH: 30
 / TYPE: DNA
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Protein
 / US-10-098-2638-7164

QY 7 TTTTATATGCTGCTGCTGCT 25
 TB 6 TTTTATATGCTGCTGCTGCT 24

RESULT 3
 US-09-801-274-740
 / Sequence 740, Application US/09801274
 / Patent No. US2002032119A1
 / GENERAL INFORMATION:
 / APPLICANT: Ireland, Michele
 / APPLICANT: Ireland, James S.
 / APPLICANT: Lander, Eric S.
 / TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 / FILE REFERENCE: 2825,2002,001
 / CURRENT APPLICATION NUMBER: US/09/801,274
 / CURRENT FILING DATE: 2001-03-07
 / PRIORITY APPLICATION NUMBER: US 60/197,510
 / PRIORITY FILING DATE: 2000-03-07
 / NUMBER OF SEQ ID NOS: 139
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 740
 / LENGTH: 31
 / TYPE: DNA
 / ORGANISM: Homo sapiens
 / US-09-801-274-740

Query Match 56.8%, Score 14.2, DB 10, Length 31,
 Best Local Similarity 76.2%, Freq. No. 9.3e+03,
 Matches 16, Conservative 1, Mismatches 4, Indels 0, Gaps 0

QY 4 TTTTATATGCTGCTGCTGCT 24
 TB 1 TTTTATATGCTGCTGCTGCT 21

RESULT 4
 US-10-098-2638-7163
 / Sequence 7163, Application US/100982638
 / Publication No. US2002032119A1
 / GENERAL INFORMATION:
 / APPLICANT: Millman, Michael
 / TITLE OF INVENTION: HUMAN MICRORNA
 / FILE REFERENCE: 3118.1

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Page 5

236	11-4	45-6	06	15	15-10	014	000	34	Sequence 38, Affi
237	11-4	45-6	06	15	15-10	014	000	40	Sequence 40, Affi
238	11-4	45-6	06	15	15-10	014	000	46	Sequence 42, Affi
239	11-4	45-6	06	15	15-10	014	000	52	Sequence 44, Affi
240	11-4	45-6	06	15	15-10	014	000	58	Sequence 46, Affi
241	11-4	45-6	06	15	15-10	014	000	64	Sequence 48, Affi
242	11-4	45-6	06	15	15-10	014	000	70	Sequence 50, Affi
243	11-4	45-6	06	15	15-10	014	000	76	Sequence 52, Affi
244	11-4	45-6	06	15	15-10	014	000	82	Sequence 54, Affi
245	11-4	45-6	06	15	15-10	014	000	88	Sequence 56, Affi
246	11-4	45-6	06	15	15-10	014	000	94	Sequence 58, Affi
247	11-4	45-6	06	15	15-10	014	000	100	Sequence 60, Affi
248	11-4	45-6	06	15	15-10	014	000	106	Sequence 62, Affi
249	11-4	45-6	06	15	15-10	014	000	112	Sequence 64, Affi
250	11-4	45-6	06	15	15-10	014	000	118	Sequence 66, Affi
251	11-4	45-6	06	15	15-10	014	000	124	Sequence 68, Affi
252	11-4	45-6	06	15	15-10	014	000	130	Sequence 70, Affi
253	11-4	45-6	06	15	15-10	014	000	136	Sequence 72, Affi
254	11-4	45-6	06	15	15-10	014	000	142	Sequence 74, Affi
255	11-4	45-6	06	15	15-10	014	000	148	Sequence 76, Affi
256	11-4	45-6	06	15	15-10	014	000	154	Sequence 78, Affi
257	11-4	45-6	06	15	15-10	014	000	160	Sequence 80, Affi
258	11-4	45-6	06	15	15-10	014	000	166	Sequence 82, Affi
259	11-4	45-6	06	15	15-10	014	000	172	Sequence 84, Affi
260	11-4	45-6	06	15	15-10	014	000	178	Sequence 86, Affi
261	11-4	45-6	06	15	15-10	014	000	184	Sequence 88, Affi
262	11-4	45-6	06	15	15-10	014	000	190	Sequence 90, Affi
263	11-4	45-6	06	15	15-10	014	000	196	Sequence 92, Affi
264	11-4	45-6	06	15	15-10	014	000	202	Sequence 94, Affi
265	11-4	45-6	06	15	15-10	014	000	208	Sequence 96, Affi
266	11-4	45-6	06	15	15-10	014	000	214	Sequence 98, Affi
267	11-4	45-6	06	15	15-10	014	000	220	Sequence 100, Affi
268	11-4	45-6	06	15	15-10	014	000	226	Sequence 102, Affi
269	11-4	45-6	06	15	15-10	014	000	232	Sequence 104, Affi
270	11-4	45-6	06	15	15-10	014	000	238	Sequence 106, Affi
271	11-4	45-6	06	15	15-10	014	000	244	Sequence 108, Affi
272	11-4	45-6	06	15	15-10	014	000	250	Sequence 110, Affi
273	11-4	45-6	06	15	15-10	014	000	256	Sequence 112, Affi
274	11-4	45-6	06	15	15-10	014	000	262	Sequence 114, Affi
275	11-4	45-6	06	15	15-10	014	000	268	Sequence 116, Affi
276	11-4	45-6	06	15	15-10	014	000	274	Sequence 118, Affi
277	11-4	45-6	06	15	15-10	014	000	280	Sequence 120, Affi
278	11-4	45-6	06	15	15-10	014	000	286	Sequence 122, Affi
279	11-4	45-6	06	15	15-10	014	000	292	Sequence 124, Affi
280	11-4	45-6	06	15	15-10	014	000	298	Sequence 126, Affi
281	11-4	45-6	06	15	15-10	014	000	304	Sequence 128, Affi
282	11-4	45-6	06	15	15-10	014	000	310	Sequence 130, Affi
283	11-4	45-6	06	15	15-10	014	000	316	Sequence 132, Affi
284	11-4	45-6	06	15	15-10	014	000	322	Sequence 134, Affi
285	11-4	45-6	06	15	15-10	014	000	328	Sequence 136, Affi
286	11-4	45-6	06	15	15-10	014	000	334	Sequence 138, Affi
287	11-4	45-6	06	15	15-10	014	000	340	Sequence 140, Affi
288	11-4	45-6	06	15	15-10	014	000	346	Sequence 142, Affi
289	11-4	45-6	06	15	15-10	014	000	352	Sequence 144, Affi
290	11-4	45-6	06	15	15-10	014	000	358	Sequence 146, Affi
291	11-4	45-6	06	15	15-10	014	000	364	Sequence 148, Affi
292	11-4	45-6	06	15	15-10	014	000	370	Sequence 150, Affi
293	11-4	45-6	06	15	15-10	014	000	376	Sequence 152, Affi
294	11-4	45-6	06	15	15-10	014	000	382	Sequence 154, Affi
295	11-4	45-6	06	15	15-10	014	000	388	Sequence 156, Affi
296	11-4	45-6	06	15	15-10	014	000	394	Sequence 158, Affi
297	11-4	45-6	06	15	15-10	014	000	400	Sequence 160, Affi
298	11-4	45-6	06	15	15-10	014	000	406	Sequence 162, Affi
299	11-4	45-6	06	15	15-10	014	000	412	Sequence 164, Affi
300	11-4	45-6	06	15	15-10	014	000	418	Sequence 166, Affi
301	11-4	45-6	06	15	15-10	014	000	424	Sequence 168, Affi
302	11-4	45-6	06	15	15-10	014	000	430	Sequence 170, Affi
303	11-4	45-6	06	15	15-10	014	000	436	Sequence 172, Affi
304	11-4	45-6	06	15	15-10	014	000	442	Sequence 174, Affi
305	11-4	45-6	06	15	15-10	014	000	448	Sequence 176, Affi
306	11-4	45-6	06	15	15-10	014	000	454	Sequence 178, Affi
307	11-4	45-6	06	15	15-10	014	000	460	Sequence 180, Affi
308	11-4	45-6	06	15	15-10	014	000	466	Sequence 182, Affi



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us-09-890-363-6.max.mli

QY 2 TTCTTTCTATGCTGTGTTG 22
DB 5 TTCACTCTTATGCTGTGTTG 25

RESULT 39
US-09-890-363-6
Sequence 37, Application US/02-247190
Patent No. 6214549
GENERAL INFORMATION:
APPLICANT: Szoostak, Jack W.
APPLICANT: Fawcett, Richard W.
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
FILE REFERENCE: 00786/350005
CURRENT FILING DATE: US/09/247,190
CURRENT APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1999-02-09
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
EARLIER APPLICATION NUMBER: 09/007,005
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 37
LENGTH: 26
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES: DNA splint
OTHER INFORMATION: n = a, t, c, or g.
US-09-247-190-37

Query Match 52.0%; Score 13; DB 4; Length 26;
Best Local Similarity 72.7%; Freq. No 3.7e+03;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 TTCTTTCTATGCTGTGTTG 24
DB 1 TTCTTTCTATGCTGTGTTG 22

RESULT 40
US-09-051-079-1
Sequence 1, Application US/09051079A
Patent No. 6214549
GENERAL INFORMATION:
APPLICANT: WEINDEL, Kurt
APPLICANT: TASSON, R. Richard
TITLE OF INVENTION: METHOD OF DETECTING A SUBSTANCE BY AN ANALYZED
FILE REFERENCE: 101614-07096
CURRENT FILING DATE: US/09/051,079A
CURRENT APPLICATION NUMBER: PCT/EP96/04358
EARLIER FILING DATE: 1996-09-10
EARLIER APPLICATION NUMBER: DE/195 37 952.7
EARLIER FILING DATE: 1995-10-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 1
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES: misc. binding
NAME/KEY: (1)-(27)
LOCATION: (1)-(27)
OTHER INFORMATION: The symbol n means a amino acid, elongated
OTHER INFORMATION: bound the symbol n means a amino acid and labeled with

OTHER INFORMATION: digoxigenin N-hydroxy succinimide-ester.
FEATURE: Description of Artificial Sequence:
OTHER INFORMATION: digoxigenin N-hydroxy succinimide-ester
US-09-051-079-1

Query Match 52.0%; Score 13; DB 4; Length 27;
Best Local Similarity 69.6%; Freq. No 3.7e+03;
Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 2 TTCTTTCTATGCTGTGTTG 24
DB 1 TTCTTTCTATGCTGTGTTG 23

Search completed: July 21, 2003, 15:49:28
Cpu time: 26.1617 secs

ZIP: 20005
 COMPUTER READABLE FORM
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/779,335
 FILING DATE: 06-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/779,333
 FILING DATE: 03-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: KILLIP, David J.
 REGISTRATION NUMBER: 36,576
 REFERENCE/DOCKET NUMBER: 4000001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202)628-8844
 TELEFAX: (202)628-8844
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US 08 779 335 17

Query Match 52.0%, Score 13, DB 3, Length 25,
 Best Local Similarity 76.2%, Pct. No. 3.7e+03,
 Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0.

QY 2 TTTCTTCTATGTTCTTCTG 22
 DB 5 TACTTATCTATGTTCTTCTG 25

RESULT 37
 US 08 938 835A-17
 Sequence 17, Application US/08938835A
 Patent No. 6060245
 GENERAL INFORMATION:
 APPLICANT: SORCE, Joseph A.
 APPLICANT: WILLIAMS, Rebecca L.
 TITLE OF INVENTION: METHODS AND MATERIALS FOR GENERATING
 TITLE OF INVENTION: SPECIFIC NUCLEOTIC ACID SEQUENCES
 NUMBER OF SEQUENCES: 64
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fungoan, Hendelsohn, Fairlaw, Garselli &
 STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3115
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.2
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/779,335A
 FILING DATE: 26-SEPT-1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/779,333
 FILING DATE: 03-JAN-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/779,335
 FILING DATE: 06-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barker, M. Paul

REGISTRATION NUMBER: 32,013
 REFERENCE/DOCKET NUMBER: 04001 0044 02000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-08-938-835A-17

Query Match 52.0%, Score 13, DB 3, Length 25,
 Best Local Similarity 76.2%, Pct. No. 3.7e+03,
 Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0.

QY 2 TTTCTTCTATGTTCTTCTG 22
 DB 5 TACTTATCTATGTTCTTCTG 25

RESULT 38
 PCT-US94-14096-6

Sequence 6, Application PCT/US9414096
 GENERAL INFORMATION:
 APPLICANT: NIKIFOROV, THEO
 APPLICANT: KNAPP, MICHAEL
 TITLE OF INVENTION: METHOD FOR THE IMMUTILIZATION OF NUCLEIC
 TITLE OF INVENTION: ACID MOLECULES
 NUMBER OF SEQUENCES: 24
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWREY & SIMON
 STREET: 1299 PENNSYLVANIA AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/14096
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: AUERBACH, JEFFREY I.
 REGISTRATION NUMBER: 32,680
 REFERENCE/DOCKET NUMBER: 639-106
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 383-7451
 TELEFAX: (202) 383-6610
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Equus caballus
 IMMEDIATE SOURCE:
 CLONE: 680
 PCT-US94-14096-6

Query Match 52.0%, Score 13, DB 3, Length 25,
 Best Local Similarity 76.2%, Pct. No. 3.7e+03,
 Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0.

ADDRESSEE: EMBOLD, MERRILL, ESMITH & IRELAND PLLC
STREET: 1200 G Street N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA

CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-4415
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICANT NAME: US-09-890-363-6
 FILING DATE: 26 SEPT 1997
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/775,702
 FILING DATE: 03 JAN 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/779,335
 FILING DATE: 06-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barker, M. Paul
 REGISTRATION NUMBER: 35,013
 REFERENCE/DOCKET NUMBER: 641-1 0044 00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 30:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 US-09-890-363-6
 Locality Match: 5.8% Score 13.2, DE 3, Length 20
 Best Local Similarity: 98.3%, Pct. ID: 30.03, 4: Indels 0, Gaps 0
 Matches: 15: Conservative 0, Mismatches 4: Indels 0, Gaps 0
 0Y 4 CTTTCTTCTTCTTCTG 13 11
 10 2 CTTTCTTCTTCTTCTG 20

RESULT 32
 US-09-890-363-6
 Sequence 4, Application US/0879335
 Patent No. 6218523
 GENERAL INFORMATION:
 APPLICANT: French, Cynthia K.
 APPLICANT: Schneider, Patrick A.
 APPLICANT: Yamamoto, Karen K.
 TITLE OF INVENTION: Prostate Cancer Specific Marker
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Potreroadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/776,315
 FILING DATE: 06 MAR 1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/047,811
 FILING DATE: 15 MAY 1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 60/041,246
 FILING DATE: 07 MAR 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Storella, John R.
 REGISTRATION NUMBER: 22,944
 REFERENCE/DOCKET NUMBER: 019002 0002005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 FEATURE:
 NAME/KEY: 1 30
 LOCATION: 1 30
 OTHER INFORMATION: /not a "4" on 130 (3485) Lower Primer
 US-09-890-363-6
 Locality Match: 5.8% Score 13.2, DE 4, Length 30
 Best Local Similarity: 83.3%, Pct. ID: 31.6+03
 Matches: 15: Conservative 0, Mismatches 4: Indels 0, Gaps 0
 0Y 1 TTTCTTTCTTCTTCTG 18
 10 12 TTTCTTTCTTCTTCTG 29

RESULT 33
 US-08-779-355-4
 Sequence 4, Application US/0879355
 Patent No. 6017701
 GENERAL INFORMATION:
 APPLICANT: Sauer, Joseph A.
 APPLICANT: Mullins, Rebecca L.
 TITLE OF INVENTION: WEIGHTED AVERAGE FOR GENERATING
 NUMBER OF SEQUENCES: 35
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evenson, McKean, Edwards & Lennihan P.C.,
 STREET: 1200 G Street N.W., Suite 700
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/779,355
 FILING DATE: 06-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/775,993
 FILING DATE: 03-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kulik, David J.
 REGISTRATION NUMBER: 36,576
 REFERENCE/DOCKET NUMBER: 43992CP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/068,478
FILING DATE: 26 OCT 1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29 MAR 1993
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/858,747
FILING DATE: 27 MAR 1992
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026 4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO:

101.
SEQUENCE CHARACTERISTICS:
LENGTH: 31 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR

US-09-890-478-101

Query Match 53.6% Score 13.4; DR 2; Length 41;
Best Local Similarity 73.98; Pred No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TTTCTTTGATGCTCTGCTG 24
TTCTTTCTTTGATGCTGCTG 1

no 23 TTTCTTTGATGCTGCTG 1

RESULT 27
US-09-414-117-101/c

Sequence 101, Application US/09/414117
Patent No. 6291664
GENERAL INFORMATION:

APPLICANT:

ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/414,117

FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/859,049
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29 MAR-1993
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/858,747
FILING DATE: 27 MAR 1992
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2026 4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO:

101:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR

US-09-414-117-101

Query Match 53.6% Score 13.4; DR 4; Length 41;
Best Local Similarity 73.98; Pred No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 TTTCTTTGATGCTCTGCTG 24
TTCTTTCTTTGATGCTGCTG 1

no 23 TTTCTTTGATGCTGCTG 1

RESULT 28
US-09-678-437-101/c

Sequence 101, Application US/09/678437
Patent No. 6414132
GENERAL INFORMATION:

APPLICANT:

ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/678,437
FILING DATE: 02-OCT-2000
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/850,949
FILING DATE: <Unknown>
APPLICATION NUMBER: PCT/US93/02908
FILING DATE: 29-MAR-1993
APPLICATION NUMBER: US 07/858,747
FILING DATE: 27 MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398

```

US-08-850-049-101/C
Sequence 101, Application US/08850049
Patent No. 5965726
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130
CORRESPONDENCE ADDRESS:
ADDRESS: MURKIN & FINEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
TEXT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,473
FILING DATE: 02-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/050,478
FILING DATE: 26-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: ECT/0203/02908
FILING DATE: 29-MAR 1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 07/858,747
FILING DATE: 27 MAR-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MORRY, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2096-4006US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 31 BASE PAIRS
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
US-08-850-049-101
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Seq Match 59.6% Score 13.4; Dh 2;
Rest Local Similarity 73.3% T64 No 2,be+03;
Matches 17; Conservative b; Inters 0; Gaps
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CY 2 TTTCTTCTATGCTGCTGTTG 24
||||| ||| ||| |||
DB 23 TTTTCTCTGTATGTTGTTG 1
||||| ||| ||| |||
---
RESULT 26
US-08-050-478-101/C
Sequence 101, Application US/08050478
Patent No. 5972596
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: METHOD OF ELIMINATING
TITLE OF INVENTION: INHIBITORY/INSTABILITY REGIONS OF mRNA
NUMBER OF SEQUENCES: 130

```

```

STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10203
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07 JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29 NOV 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24 MAR 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02 SEP 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,104
FILING DATE: 16 SEP 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,104
FILING DATE: 16 SEP 1994
ATTORNEY/AGENT INFORMATION:
NAME: Immen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24844-100347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 962 4810
TELEFAX: 202 962 8450
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10203-71

Query Match 54.4%; Score 13.6; DB 5; Length 30;
Best Local Similarity 80.0%; Pseq No 2 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

RESULT 23
PCT-US95-10203-71

```

Sequence 71, Application PC/TUS9510203
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Hartman, Keith E.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.

```

db 8 TTTCTTTTATATATTTT 20
8 TTTCTTTTATATATTTT 27

```

APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSER: Venable, Baetjer, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10203
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 07 JUN 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24 MAR 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29 NOV 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,104
FILING DATE: 16 SEP 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02 SEP 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/398,104
FILING DATE: 16 SEP 1994
ATTORNEY/AGENT INFORMATION:
NAME: Immen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24844-100347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 962 4810
TELEFAX: 202 962 8450
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
PCT-US95-10203-71

Query Match 54.4%; Score 13.6; DB 5; Length 30;
Best Local Similarity 80.0%; Pseq No 2 1e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

RESULT 24

```

PCT-US95-10220-71
Sequence 71, Application PC/TUS9510220
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio

```

db 1 TTTCTTTTATATATTTT 20
8 TTTCTTTTATATATTTT 27

Page 15

```

1 ADDRESS: Venable, Baetjer, Howard & Civiletti, LLP
2 STREET: 1201 New York Avenue, N.W., Suite 1000
3 CITY: Washington
4 STATE: DC
5 COUNTRY: USA
6 ZIP: 20005
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: floppy disk
9 COMPILER: IBM PC compatible
10 OPERATING SYSTEM: PC-DOS/MS-DOS
11 SOFTWARE: PatentIn Release #1.0, Version #1.10
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/08/366,727
14 FILING DATE:
15 CLASSIFICATION:
16 PRIOR APPLICATION DATA:
17 APPLICATION NUMBER: US 08/483,554
18 FILING DATE: 07-JUN-1995
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: US 08/348,824
21 FILING DATE: 09-NOV-1994
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: US 08/369,104
24 FILING DATE: 16-SEP-1994
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: US 08/790,266
27 FILING DATE: 02-SEP-1994
28 PRIOR APPLICATION DATA:
29 APPLICATION NUMBER: US 08/737,221
30 FILING DATE: 12-APR-1994
31 ATTORNEY/AGENT INFORMATION:
32 NAME: Ihnen, Jeffrey L.
33 REGISTRATION NUMBER: 28,957
34 REFERENCE/DOCKET NUMBER: 24894-1-1347
35 TELECOMMUNICATION INFORMATION:
36 TELEPHONE: 202-362-8400
37 TELEFAX: 202-362-8400
38 INFORMATION FOR SEQ ID NO. 71:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 30 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44 MOLECULE TYPE: DNA (genomic)
45 HYPOTHEetical: NO
46 ORIGINAL SOURCE:
47 ORGANISM: Homo sapiens
48
49 US-08-850-727-71
50
51 Query Match 54.4% Score 13.6, DB 4, length 30;
52 Best Local Similarity 80.0%, Freq No. 2, 1e+01;
53 Matches 16, Conservative 0, Mismatches 4, Index 0, Gaps 0
54
55 QY 1 TTCTCTTCTATGCTCT 20
56 DB 8 TGTCTTCTATGATCTCT 27
57
58 RESULT 22
59 PC-0855-10322-71
60 Sequence 71, Application PC/TUS551u02
61 GENERAL INFORMATION:
62 APPLICANT: Shattuck-Bidens, Donna M.
63 APPLICANT: Simard, Jacques
64 APPLICANT: Emi, Mitsuru
65 APPLICANT: Nakamura, Yutake
66 APPLICANT: Duracher, Francine
67 TITLE OF INVENTION: In vivo Mutations and Polymorphisms
68 TITLE OF INVENTION: in the 17q-Linked Breast and Ovarian Cancer
69 TITLE OF INVENTION: Susceptibility Gene
70 NUMBER OF SEQUENCES: 85
71 REPRESENTATIVE ACCESS:
72 ADDRESS: Venable, Baetjer, Howard & Civiletti, LLP

```

```

APPLICATION NUMBER: US/08/487,007
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,201
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.962.4810
TELEFAX: 202.962.8300
INFORMATION FOR SEQ ID NO: 71
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA (poly-A)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-487-007-71

Query Match: 54.4%; Score 13.6; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 2; Id=03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 TTCTTTTCATATGCTCTT 20
      |||||
      8 TGCTTTTCATATGCTCTT 27

RESULT 19
US-08-483-5548-71
Sequence 71, Application US/084835548
Patent No. 5747282
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venables, Baglioni, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

```

```

COMPUTER-IBM PC compatible
OPERATING SYSTEM: PC-TOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,554B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/409,305
FILING DATE: 24-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/348,824
FILING DATE: 29-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,104
FILING DATE: 16-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/300,266
FILING DATE: 02-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,201
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ihnen, Jeffrey L.
REGISTRATION NUMBER: 28,957
REFERENCE/DOCKET NUMBER: 24884-109147
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202.962.4810
TELEFAX: 202.962.8300
INFORMATION FOR SEQ ID NO: 71
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-483-5548-71

Query Match: 54.4%; Score 13.6; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 2; Id=03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 TTCTTTTCATATGCTCTT 20
      |||||
      8 TGCTTTTCATATGCTCTT 27

RESULT 20
US-08-488-0118-71
Sequence 71, Application US/084880118
Patent No. 5753441
GENERAL INFORMATION:
APPLICANT: Skolnick, Mark H.
APPLICANT: Goldgar, David E.
APPLICANT: Miki, Yoshio
APPLICANT: Swenson, Jeff
APPLICANT: Kamb, Alexander
APPLICANT: Harshman, Keith D.
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Tavtigian, Sean V.
APPLICANT: Wiseman, Roger W.
APPLICANT: Futreal, P. Andrew
TITLE OF INVENTION: 17q Linked Breast and Ovarian Cancer
TITLE OF INVENTION: Susceptibility Gene
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Venables, Baglioni, Howard & Civiletti, LLP
STREET: 1201 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05-06-1994-005
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 05-06-1994-005
FILING DATE: 24 MAR-1995
PTECH APPLICATION DATA:
APPLICATION NUMBER: US 06/348,824
FILING DATE: 28 SEP 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/308,104
FILING DATE: 18 SEP 1994
PTECH APPLICATION DATA:
APPLICATION NUMBER: US 06/308,266
FILING DATE: 02 SEP 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/308,221
FILING DATE: 12 AUG-1994
APPLICANT/AGENT INFORMATION:
NAME: Ibram, Jeffrey L.
REGISTRATION NUMBER: 29,957
REFERENCE/DOCKET NUMBER: 28864-103347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-662-4411
TELEFAX: 202-662-4411
INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-29 493 573-71

ENTRY March 54.4% SCORE 13.0? DB 1? Length 30?
Best Local Similarity 80.0% Prod No 2 1e+03?
Mismatch 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0

CY 1 TTTCTTTCAAGCTCTCT 20
1 |||||
DB 8 TTTCTTTCAAGCTCT 27

RESULT 18
US-08-487-002-71
US-08-487-002-71
Patent No. 5710001
GENERAL INFORMATION:
APPLICANT: Shattuck-Eidens, Donna M.
APPLICANT: Simard, Jacques
APPLICANT: Eml, Mitsuru
APPLICANT: Nakamura, Yusuke
APPLICANT: Durochet, Françoise
TITLE OF INVENTION: 17q-linked Direct and Ovarian Cancer
TITLE OF INVENTION: p53-linked Direct and Ovarian Cancer
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSER: Warrilo, Patricia, Howard S. Giffels, LLP
STREET: 101 New York Avenue, N.W., Suite 1000
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS 5.0
SOFTWARE: GenBank Release #100, Version #1.30
CURRENT APPLICATION DATA:

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Sequence 10, Application US/08791883
 Patent No. 5879890
 GENERAL INFORMATION:
 APPLICANT: LAKEN, STEVE
 APPLICANT: GRUBER, STEPHEN
 APPLICANT: PERBERN, GIORIA
 APPLICANT: KINTNER, KENNETH
 APPLICANT: VOGELSTEIN, BEPT
 TITLE OF INVENTION: APOPTATION ASSOCIATED WITH
 TITLE OF INVENTION: FAMILIAL COLONIAL CANCER IN ASHERNATI JEWS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bahner & Mitcoff, Ltd.
 STREET: 1001 G Street, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08791,883
 FILING DATE: 31-JAN-1997
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A
 REGISTRATION NUMBER: 32,145
 REFERENCE/DOCKET NUMBER: 01107 03734
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 97430 BMR UT
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-791 883-10

Query Match 54.4% Score 13.6, DB 2, Length 25,
 First Local Similarity 40.0%, Fred No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 TTTCTTTTATTTCTTTT 20
 DB 21 TTTCTTTTCTCTATT 2

RESULT 17
 US-09-023-673-1073
 Sequence 10, Application US/08791883
 Patent No. 5879890
 GENERAL INFORMATION:
 APPLICANT: LAKEN, STEVE
 APPLICANT: GRUBER, STEPHEN
 APPLICANT: PERBERN, GIORIA
 APPLICANT: KINTNER, KENNETH
 APPLICANT: VOGELSTEIN, BEPT
 TITLE OF INVENTION: APOPTATION ASSOCIATED WITH
 TITLE OF INVENTION: FAMILIAL COLONIAL CANCER IN ASHERNATI JEWS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Bahner & Mitcoff, Ltd.
 STREET: 1001 G Street, N.W.
 CITY: Washington
 STATE: DC

COUNTRY: USA
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08791,883
 FILING DATE:
 CLASSIFICATION:
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/791,883
 FILING DATE: 31-JAN-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Kagan, Sarah A
 REGISTRATION NUMBER: 32,145
 REFERENCE/DOCKET NUMBER: 01107 03734
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-508-9100
 TELEFAX: 202-508-9299
 TELEX: 97430 BMR UT
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-09-023-673-10

Query Match 54.4% Score 13.6, DB 3, Length 25,
 First Local Similarity 40.0%, Fred No. 2.1e+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 TTTCTTTTATTTCTTTT 20
 DB 21 TTTCTTTTCTCTATT 2

RESULT 16
 US-08-480-784-71
 Sequence 7, Application US/08480784
 Patent No. 5693473
 GENERAL INFORMATION:
 APPLICANT: Skolnick, Mark H.
 APPLICANT: Goldfarb, David E.
 APPLICANT: Miki, Yoshio
 APPLICANT: Swenson, Jeff
 APPLICANT: Lamb, Alexander
 APPLICANT: Harshman, Keith D.
 APPLICANT: Shattuck-Fidens, Donna M.
 APPLICANT: Tavtigian, Sean V.
 APPLICANT: Wiseman, Roger W.
 APPLICANT: Futreal, P. Andrew
 TITLE OF INVENTION: 17q-linked Proser and Ovarian Cancer
 TITLE OF INVENTION: Susceptibility Gene
 NUMBER OF SEQUENCES: 85
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti, LLP
 STREET: 1201 New York Avenue, N.W., Suite 1000
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Folioase #10, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/480,784
 FILING DATE:
 CLASSIFICATION: 435

SEQ ID NO: 34
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide Sequence
US-08-864-473-34

Query Match: 55.2% Score 13.8; DB 3; Length 21;
Best Local Similarity: 88.2%; Pred. No. 1.7e+03;
Matches: 15; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

QY 2 TTTCTTCTATGCTG 18
DB 18 TTTCTTCTTCTGCTG 2

RESULT 8
US-08-864-473-36/C
Sequence 36, Application US/08864473
Patent No. 6027889
GENERAL INFORMATION:
APPLICANT: Barany, Francis
APPLICANT: Lubin, Matthew
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING
TITLE OF INVENTION: COMPLEX IMAGE DETECTION AND POLYMERASE CHAIN REACTION
FILE REFERENCE: 19603/441
CURRENT APPLICATION NUMBER: US/08/864,473
CURRENT FILING DATE: 1999-11-15
EARLIER APPLICATION NUMBER: 60/018,532
EARLIER FILING DATE: 1996-05-29
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 36
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide Sequence
US-08-864-473-36

Query Match: 55.2% Score 13.8; DB 3; Length 21;
Best Local Similarity: 88.2%; Pred. No. 1.7e+03;
Matches: 15; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

QY 2 TTTCTTCTATGCTG 18
DB 18 TTTCTTCTTCTGCTG 2

RESULT 9
US-09-440-523-34/C
Sequence 34, Application US/09440523
Patent No. 6268148
GENERAL INFORMATION:
APPLICANT: Barany, Francis
APPLICANT: Lubin, Matthew
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING
TITLE OF INVENTION: COMPLEX IMAGE DETECTION AND POLYMERASE CHAIN REACTION
FILE REFERENCE: 19603/441
CURRENT APPLICATION NUMBER: US/09/440,523
CURRENT FILING DATE: 1997-11-15
PRIOR APPLICATION NUMBER: 08/864,473
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 34
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:

OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide Sequence
US-09-440-523-34

Query Match: 55.2% Score 13.8; DB 4; Length 21;
Best Local Similarity: 88.2%; Pred. No. 1.7e+03;
Matches: 15; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

QY 2 TTTCTTCTATGCTG 18
DB 18 TTTCTTCTTCTGCTG 2

RESULT 10
US-09-440-523-36/C
Sequence 36, Application US/09440523
Patent No. 6268148
GENERAL INFORMATION:
APPLICANT: Barany, Francis
APPLICANT: Lubin, Matthew
TITLE OF INVENTION: DETECTION OF NUCLEIC ACID SEQUENCE DIFFERENCES USING
TITLE OF INVENTION: COMPLEX IMAGE DETECTION AND POLYMERASE CHAIN REACTION
FILE REFERENCE: 19603/441
CURRENT APPLICATION NUMBER: US/09/440,523
CURRENT FILING DATE: 1999-11-15
PRIOR APPLICATION NUMBER: 08/864,473
PRIOR FILING DATE: 1997-05-28
NUMBER OF SEQ ID NOS: 76
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO: 36
LENGTH: 21
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide Sequence
US-09-440-523-36

Query Match: 55.2% Score 13.8; DB 4; Length 21;
Best Local Similarity: 88.2%; Pred. No. 1.7e+03;
Matches: 15; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

QY 2 TTTCTTCTATGCTG 18
DB 18 TTTCTTCTTCTGCTG 2

RESULT 11
US-08-117-952-23/C
Sequence 23, Application US/08117052
Patent No. 5851760
GENERAL INFORMATION:
APPLICANT: Evans, Glen A.
APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
NMAP OF SEQUENCES: 797
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Buergemann & Clark
CITY: 444 South Flower Street, Suite 2000
STATE: CA
COUNTRY: USA
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
CLASSIFICATION: 435

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1  ZIP: 20004
2  COMPUTER READABLE FORM.
3  MEDIUM TYPE: Floppy disk
4  COMPUTER: IBM PC compatible
5  OPERATING SYSTEM: PC DOS/MS-DOS
6  SOFTWARE: Patent Release #1.0, Version #1.25
7  CURRENT APPLICATION DATA:
8  APPLICATION NUMBER: US/09/241,149
9  FILING DATE:
10 CLASSIFICATION: 435
11 ATTORNEY/AGENT INFORMATION:
12 NAME: ABERBACH, JEFFREY I
13 RESISTANCE NUMBER: 32,499
14 REFERENCE/DOCKET NUMBER: 639-105
15 TELECOMMUNICATION INFORMATION:
16 TELEPHONE: (202) 383 7451
17 TELEFAX: (202) 392 6610
18 INFORMATION FOR SEQ ID NO. 9:
19 SEQUENCE CHARACTERISTICS:
20 LENGTH: 30 base pairs
21 TYPE: nucleic acid
22 STRANDEDNESS: single
23 TOPOLOGY: linear
24 MOLECULE TYPE: DNA (genomic)
25 HYPOTHETICAL: NO
26 ANTI-SENSE: NO
27 ORIGINAL SOURCE:
28 ORGANISM: Equus caballus
29 IMMEDIATE SOURCE:
30 CLONE: 1210
31 US-09-341-148-9
32
33 Query March 56.0% Score 14 DB 11 Length 30
34 Best Local Similarity 77.3% Pval No 1.5e+03
35 Matches 17, Conservative 0, Mismatches 1, Indels 0, Gaps 0
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977 10.2 40.8 32 3 US-09-829-912-2 Sequence 2, Appl:
978 10.2 40.8 32 4 US-08-974-549A-589 Sequence 589, App:
979 10.2 40.8 32 4 US-08-975-836C-99 Sequence 99, Appl:
980 10.2 40.8 32 4 US-08-974-549-104 Sequence 104, App:
981 10.2 40.8 32 4 US-09-438-323-109 Sequence 109, App:
982 10.2 40.8 32 5 PCT-US99-01194-3 Sequence 3, Appl:
983 10.2 40.8 33 1 US-08-314-309A-16 Sequence 16, Appl:
984 10.2 40.8 33 1 US-08-314-309A-32 Sequence 32, Appl:
985 10.2 40.8 33 2 US-08-411-607A-5 Sequence 5, Appl:
986 10.2 40.8 33 3 US-08-883-616-1 Sequence 1, Appl:
987 10.2 40.8 33 3 US-09-038-741-4 Sequence 4, Appl:
988 10.2 40.8 33 3 US-08-631-319A-2 Sequence 2, Appl:
989 10.2 40.8 33 3 US-08-882-540-18 Sequence 18, Appl:
990 10.2 40.8 33 4 US-08-208-084-70 Sequence 70, Appl:
991 10.2 40.8 33 4 US-03-448-524-35 Sequence 35, Appl:
992 10.2 40.8 33 4 US-09-426-332-5 Sequence 5, Appl:
993 10.2 40.8 33 4 US-08-842-106E-14 Sequence 14, Appl:
994 10.2 40.8 33 4 US-08-948-318-14 Sequence 14, Appl:
995 10.2 40.8 33 4 US-09-712-266-16 Sequence 16, Appl:
996 10.2 40.8 33 4 US-09-354-231B-26 Sequence 26, Appl:
997 10.2 40.8 33 4 US-09-603-043-19 Sequence 19, Appl:
998 10.2 40.8 33 4 US-03-128-604E-16 Sequence 16, Appl:
999 10.2 40.8 33 4 US-08-771-212A-11 Sequence 11, Appl:
1000 10.2 40.8 33 5 PCT-US94-03796-3 Sequence 3, Appl:

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ALIGNMENTS

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RESULT 1
US-09-157-177-66/c
Sequence 66, Application US/09157177
Patent No. 6039398
GENERAL INFORMATION:
APPLICANT: Butler, John M.
APPLICANT: Li, Jia
APPLICANT: Maudon, Joseph A.
APPLICANT: Pappas, David H.
TITLE OF INVENTION: IDENTIFYING BY MASS SPECTROMETRY WITH POLYMORPHIC DNA
FILE REFERENCE: GERT-017/GERT017P
CURRENT FILING DATE: 1998-09-18
EARLIER FILING DATE: 1997-09-19
NUMBER OF SEQ. ID NOS.: 115
SOFTWARE: Patent In Ver. 2.0
SEQ. ID NO. 66
LENGTH: 24
TYPE: DNA
ORGANISM: Homo sapiens
US-09-157-177-66

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Query Match 58.41, Score 14.6, DB 3, Length 24;
Best Local Similarity 81.01, Pred. No. 9, 1e+03;
Matches 17, Conservative 0, Mismatches 4, Indels 0, Gaps 0;

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CY 5 TTTTCTATGCTGTTGTA 25
DB 21 TTTTATATTTTCTGTTTA 1

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RESULT 2
US-09-051-079-2
Sequence 2, Application US/09051079A
Patent No. 6214949
GENERAL INFORMATION:
APPLICANT: WEINDEL, RUTH
APPLICANT: SEIDEL, GRISEGH
APPLICANT: LAGGONCHY, GORDA
TITLE OF INVENTION: METHOD OF IDENTIFYING A SUBSTANCE TO BE ANALYZED
FILE REFERENCE: 101614-07096
OTHER INFORMATION: None
US-09-051-079-2

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CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PCT/EP94/04358
EARLIER FILING DATE: 1996-10-08
EARLIER APPLICATION NUMBER: SE/795 17 952.7
EARLIER FILING DATE: 1996-10-12
NUMBER OF SEQ. ID NOS.: 7
SOFTWARE: Patent In Ver. 2.1
SEQ. ID NO. 2
LENGTH: 31
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)
OTHER INFORMATION: a small gap found with PIP-TRG.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Clp has with 10.1, 11e
US-09-051-079-2

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Query Match 57.61, Score 14.4, DB 4, Length 31;
Best Local Similarity 81.7, Pred. No. 1e+03;
Matches 18, Conservative 0, Mismatches 6, Indels 0, Gaps 0;

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CY 1 TTTTCTATGCTGTTGTA 24
DB 4 TTTTATATTTTCTGTTGTA 27

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RESULT 3
US-09-560-594-89
Sequence 89, Application US/090560594
Patent No. 6245390
GENERAL INFORMATION:
APPLICANT: Lex M. Cowart
TITLE OF INVENTION: ARTISERSE WQUATION OF 21NF FIVER PROTEIN 107 EXPRESSION
FILE REFERENCE: RTS-0144
CURRENT FILING DATE: 1999-04-28
NUMBER OF SEQ. ID NOS.: 89
SEQ. ID NO. 89
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial Sequence
US-09-560-594-89

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Query Match 56.81, Score 14.2, DB 4, Length 20;
Best Local Similarity 84.21, Pred. No. 1.2e+03;
Matches 16, Conservative 0, Mismatches 3, Indels 0, Gaps 0;

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CY 3 TTTTCTATGCTGTTG 21
DB 2 TTTTATATTTTCTGTTG 20

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RESULT 4
US-08-341-148-8/c
Sequence 8, Application US/08341148
Patent No. 5610287
GENERAL INFORMATION:
APPLICANT: NIKIFOROV, THEO
APPLICANT: KNAPP, MICHAEL
TITLE OF INVENTION: METHOD FOR THE IDENTIFICATION OF NUCLEIC
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: HOMER & SIMON
STREET: 1209 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA

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[illegible]

394	10.8	41.2	23	4	US-09-092-077-07	Sequence 37, Appl	C 467	10.6	42.4	20	4	US-09-094-094-06	Sequence 56, Appl
395	10.8	41.2	23	4	US-09-092-077-08	Sequence 38, Appl	C 467	10.6	42.4	20	4	US-09-094-101-57	Sequence 57, Appl
396	10.8	41.2	24	1	US-09-092-085-08	Sequence 5, Appl	C 468	10.6	42.4	20	4	US-09-094-101-57	Sequence 58, Appl
397	10.8	41.2	24	1	US-09-092-126-14	Sequence 14, Appl	C 468	10.6	42.4	21	1	US-09-094-101-57	Sequence 59, Appl
398	10.8	41.2	24	3	US-09-094-080-00	Sequence 14, Appl	C 470	10.6	42.4	21	3	US-09-094-101-57	Sequence 60, Appl
399	10.8	41.2	24	3	US-09-094-113-44	Sequence 44, Appl	C 471	10.6	42.4	21	3	US-09-094-101-57	Sequence 61, Appl
400	10.8	41.2	24	4	US-09-094-082-09	Sequence 9, Appl	C 472	10.6	42.4	21	4	US-09-094-101-57	Sequence 62, Appl
401	10.8	41.2	25	1	US-09-094-084-13	Sequence 13, Appl	C 473	10.6	42.4	21	1	US-09-094-101-57	Sequence 63, Appl
402	10.8	41.2	25	1	US-09-094-084-13	Sequence 13, Appl	C 474	10.6	42.4	21	1	US-09-094-101-57	Sequence 64, Appl
403	10.8	41.2	25	2	US-09-094-617-13	Sequence 13, Appl	C 475	10.6	42.4	22	2	US-09-094-101-57	Sequence 65, Appl
404	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 476	10.6	42.4	22	4	US-09-094-101-57	Sequence 66, Appl
405	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 477	10.6	42.4	23	1	US-09-094-101-57	Sequence 67, Appl
406	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 478	10.6	42.4	23	1	US-09-094-101-57	Sequence 68, Appl
407	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 479	10.6	42.4	23	1	US-09-094-101-57	Sequence 69, Appl
408	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 480	10.6	42.4	23	1	US-09-094-101-57	Sequence 70, Appl
409	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 481	10.6	42.4	23	1	US-09-094-101-57	Sequence 71, Appl
410	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 482	10.6	42.4	23	1	US-09-094-101-57	Sequence 72, Appl
411	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 483	10.6	42.4	23	1	US-09-094-101-57	Sequence 73, Appl
412	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 484	10.6	42.4	23	1	US-09-094-101-57	Sequence 74, Appl
413	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 485	10.6	42.4	23	1	US-09-094-101-57	Sequence 75, Appl
414	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 486	10.6	42.4	23	1	US-09-094-101-57	Sequence 76, Appl
415	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 487	10.6	42.4	23	1	US-09-094-101-57	Sequence 77, Appl
416	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 488	10.6	42.4	23	1	US-09-094-101-57	Sequence 78, Appl
417	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 489	10.6	42.4	23	1	US-09-094-101-57	Sequence 79, Appl
418	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 490	10.6	42.4	23	1	US-09-094-101-57	Sequence 80, Appl
419	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 491	10.6	42.4	23	1	US-09-094-101-57	Sequence 81, Appl
420	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 492	10.6	42.4	23	1	US-09-094-101-57	Sequence 82, Appl
421	10.8	41.2	25	4	US-09-094-617-13	Sequence 13, Appl	C 493	10.6	42.4	23	1	US-09-094-101-57	Sequence 83, Appl
422	10.8	41.2	25										

Wed Jul 23 09:24:58 2003

us-09-890-363-6.max.mli

GenCore version 5.1.6
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GenCore - nucleic search, using sw model
July 21, 2003, 11:41:02 : Search time 19.1617 seconds
(without alignment)
400.117 Million cell up/hrs/sec

Run on: US-09-890-363-6
Title: 25
Perfect score: 1
Sequence: 1
Scoring table: IDENTITY NUC
Gapop 10.6, Gapext 1.0
44362 seqs, 15338381 residues
490442

Searched: 44362 seqs, 15338381 residues
Total number of hits satisfying chosen parameters: 490442
Minimum match length 0
Maximum DB seq length 35
Minimum match 100%

Post processing: Minimum Match 100%
Listing first 1000 summaries
Issued Patents HA.*
1: /cgm2/6/prodata/1/inn/64/COMB.seq.*
2: /cgm2/6/prodata/1/inn/64/COMB.seq.*
3: /cgm2/6/prodata/1/inn/64/COMB.seq.*
4: /cgm2/6/prodata/1/inn/64/COMB.seq.*
5: /cgm2/6/prodata/1/inn/64/COMB.seq.*
6: /cgm2/6/prodata/1/inn/64/COMB.seq.*

pred. n: is the number of results predicted by chance to have a
score greater than or equal to the total score distribution.
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	length	DB	ID	Description
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1	14.6	58.4	24	4	US-09-157-177.66	Sequence 66, Appl	
2	14.4	57.6	31	4	US-09-051-594.69	Sequence 2, Appl	
3	14.2	56.0	30	1	US-09-560-148.8	Sequence 4, Appl	
4	14	56.0	20	4	PCT-US94-148.8	Sequence 160, Appl	
5	13.8	55.2	20	4	US-09-326-186.1	Sequence 3, Appl	
6	13.8	55.2	21	4	US-08-864-413.34	Sequence 36, Appl	
7	13.8	55.2	21	4	US-09-440-523.34	Sequence 34, Appl	
8	13.8	55.2	21	4	US-09-440-523.34	Sequence 34, Appl	
9	13.8	55.2	21	4	US-09-440-523.34	Sequence 34, Appl	
10	13.8	55.2	21	4	US-09-440-523.34	Sequence 9, Appl	
11	13.6	54.4	24	2	US-08-117-947.23	Sequence 7, Appl	
12	13.6	54.4	22	1	US-08-711-842.9	Sequence 9, Appl	
13	13.6	54.4	24	2	US-09-073-671.9	Sequence 10, Appl	
14	13.6	54.4	26	3	US-08-731-883.10	Sequence 19, Appl	
15	13.6	54.4	26	3	US-09-023-873.10	Sequence 1, Appl	
16	13.6	54.4	30	1	US-08-480-794.71	Sequence 71, Appl	
17	13.6	54.4	30	1	US-08-487-002-71	Sequence 71, Appl	
18	13.6	54.4	30	1	US-08-481-554B-71	Sequence 71, Appl	
19	13.6	54.4	30	1	US-08-488-011B-71	Sequence 71, Appl	
20	13.6	54.4	30	1	US-08-480-727-71	Sequence 71, Appl	
21	13.6	54.4	30	5	PCT-US95-10202-71	Sequence 71, Appl	
22	13.6	54.4	30	5	PCT-US95-10203-71	Sequence 71, Appl	
23	13.6	54.4	30	5	PCT-US95-10220-71	Sequence 71, Appl	
24	13.6	54.4	31	5	PCT-US95-10220-71	Sequence 71, Appl	
25	13.4	53.6	31	2	US-08-087-049-101	Sequence 101, Appl	
26	13.4	53.6	31	2	US-08-087-049-101	Sequence 101, Appl	
27	13.4	53.6	31	4	US-09-141-117-101	Sequence 101, Appl	

28	53.6	31	4	US-09-678-437-101	Sequence 101, Appl
29	53.6	18	3	US-09-072-384-12	Sequence 12, Appl
30	53.6	20	3	US-09-779-355-30	Sequence 30, Appl
31	53.6	20	3	US-09-938-835A-30	Sequence 30, Appl
32	53.6	20	3	US-09-036-315-4	Sequence 4, Appl
33	53.6	20	3	US-09-779-355-4	Sequence 4, Appl
34	53.6	20	3	US-09-938-835A-4	Sequence 4, Appl
35	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
36	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
37	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
38	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
39	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
40	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
41	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
42	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
43	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
44	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
45	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
46	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
47	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
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49	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
50	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
51	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
52	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
53	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
54	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
55	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
56	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
57	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
58	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
59	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
60	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
61	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
62	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
63	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
64	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
65	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
66	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
67	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
68	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
69	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
70	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
71	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
72	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
73	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
74	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
75	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
76	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
77	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
78	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
79	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
80	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
81	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
82	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
83	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
84	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
85	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
86	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
87	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
88	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
89	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
90	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
91	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
92	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
93	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
94	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
95	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
96	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
97	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
98	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
99	53.6	20	3	US-08-341-148-6	Sequence 6, Appl
100	53.6	20	3	US-08-341-148-6	Sequence 6, Appl



CC subsequent cloning of the gene responsible for the trait, the products
 CC of the invention may also be used for treatment of prevention of the
 CC specified diseases
 XX
 SC Sequence 31 BP; 5 A; 4 C; 10 G; 11 T; 1 other;
 Query Match 54.4%, Score 13.6, DB 20; Length 31;
 Best local similarity 72.0%, Prod No 1 22.04;
 Matches 16; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 CY 1 TTTCTTTCTGATGCTGCTGCTG 22
 ||||| ||||| ||||| |||||
 DB 1 TTTCTGATGATGATGATGATGAT 22
 RESULT 39
 AAV72843
 ID AAV72843 standard; DNA; 33 BP.
 XX
 AC AAV72843;
 XX
 DT 19 FEB-1999 (first entry)
 XX
 DE Human interferon gamma 1 probe.
 XX
 KW Human; Interferon 4; IL 4; PCR primer; filter optic biosensor;
 KW detection; filter; hybridization; optical fiber; bio
 XX
 OS Synthetic.
 XX
 SN Homo sapiens.
 XX
 EX WC9850782-A2.
 XX
 PD 12-NOV 1998.
 XX
 PF 05-MAY-1998; 98MO-US09163.
 XX
 PR 05-MAY-1997; 97PS-0651203
 XX
 PA (TCTT) TUNTS COLLEGE.
 XX
 PI Ferguson JR, Healey BG, Walt DP;
 XX
 DP WPI; 1998-610511/51.
 XX
 PT Filter optic biosensor for selectively detecting oligonucleotide
 XX specific has single stranded oligonucleotide in situ hybridization
 XX zone defined as defect on end face surface of filter film.
 XX
 RS Disclosure; Page 45; 89pp; English.
 XX
 CC An optical biosensor has been developed which includes a plan optical
 CC fibre strand (10) which presents two strand end faces (16,18) as
 CC discrete fibre surfaces for illumination and emergence of light energy.
 CC Also described in the present invention are: (i) an oligonucleotide
 CC in situ hybridization zone configuration; the specific of single stranded
 CC oligonucleotide is disposed as a deposit upon the end face and serves as
 CC a defocused, single-species, fixed probe suitable for selective in situ
 CC hybridization and detection with a multi-wavelength light source; (b)
 CC hybridization (2) any complementary oligonucleotide target probe
 CC hybridized in situ ultimately bears a joined fiber-optic light probe
 CC comprising a light energy absorbing dye of known optical characteristics.
 CC The resulting specific specific, in situ hybridized oligonucleotide
 CC reacting product formed in the hybridization zone is effectively
 CC detectable via the spectral characteristics of the joined hybridizing
 CC label concomitantly disposed at the strand end face surface. The
 CC biosensor overcomes and eliminates most, if not all, of the major
 CC limitations and growth hindrances such as the problems of assay
 CC sensitivity, lengthy analysis times and the quantum of background signal
 CC noise. The present sequence represents a probe for human interferon
 CC gamma 1 from the present invention.
 XX
 SC Sequence 33 BP; 1 A; 4 C; 6 G; 22 T; 0 other;

Query Match 54.4%, Score 13.6, DB 19; Length 31;
 Best local similarity 72.0%, Prod No 1 22.04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CY 1 TTTCTTTCTGATGCTGCTGCTG 22
 ||||| ||||| ||||| |||||
 DB 1 TTTCTGATGATGATGATGATGAT 22
 RESULT 40
 ABUS6697
 ID ABUS6697 standard; DNA; 33 BP.
 XX
 AC ABUS6697;
 XX
 DT 30-JUL-2002 (first entry)
 XX
 DE PCR primer #4 for polyadenylation binding protein 20.13 cDNA.
 XX
 KW Human; polyadenylation binding protein 20.13;
 KW gene; development; disorder; growth developmental; disturbance; disease;
 KW gene therapy; PCR; primer; seq.
 XX
 OS Homo sapiens.
 XX
 EX WC0004472-A1.
 XX
 PD 01 APR 2002.
 XX
 PF 20-AUG-2001; 2001MO-CN01259.
 XX
 PR 23 AUG 2000; 2000CN-0119744.
 XX
 PA (SHAN) SHANGHAI BIOGENEUS GENE DEV INC.
 XX
 PI Mao Y, Xie Y;
 XX
 DP WPI; 2002-281267/22.
 XX
 PT New human polyadenylation binding protein 20.13 for diagnosis and
 PT treating embryonic development disorders and growth developmental
 PT disturbance diseases.
 XX
 RS Example 5; Page 18; 36pp; Chinese.
 XX
 CC The present invention relates to a method for amplifying RNA extracted from human
 CC polyadenylated binding protein 20.13, the biological and
 CC polynucleotide are used in diagnosis and treatment of embryo
 CC development disorders and growth developmental disturbance diseases.
 CC The polynucleotide may also be used for gene therapy.
 XX
 SC Sequence 33 BP; 7 A; 8 C; 8 G; 10 T; 0 other;
 Query Match 54.4%, Score 13.6, DB 24; Length 33;
 Best local similarity 72.0%, Prod No 1 22.04;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CY 1 TTTCTTTCTGATGCTGCTGCTG 22
 ||||| ||||| ||||| |||||
 DB 1 TTTCTGATGATGATGATGATGAT 22
 Search completed: 2003-07-23 09:24:58
 CPU time: 35.441 secs

CC 168 nt homopolymer equivalent, where the region contains a T to A
 CC transversion at nucleotide 1990. The method is used for determining the
 CC presence in a proband of a mutation in the APC gene associated with a
 CC family history (1) to find out if APC deficiency among Ashkenazi
 CC Jews.
 CC
 CC Sequence 24 BP; 16 A; 1 C; 4 G; 2 T; 0 other;
 CC
 CC Query Match 54.4%; Score 13.6; DB 19; Length 24;
 CC Best Local Similarity 80.0%; Prod. No. 1.9e+04;
 CC Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC 1 TTTCTTTTATGTCGTCAT 20
 CC |||||
 CC 20 TTTCTTTTATGTCGTCAT 1
 CC
 CC RESULT 34
 CC AAV43957/C
 CC ID AAV43957 standard; DNA; 25 BP.
 CC XX
 CC AC AAV43957;
 CC XX
 CC DT 26-OCT-1998 (first entry)
 CC XX
 CC DE APC mutant gene specific oligonucleotide.
 CC XX
 CC KW APC, human, oligonucleotide; CPT, chemical mutation; Ashkenazi Jew,
 CC mutation analysis; hybridization, ss.
 CC XX
 CC OS Synthetic.
 CC OS Homo sapiens.
 CC XX
 CC PN WO9833940-A1.
 CC XX
 CC PD 06-AUG-1998.
 CC XX
 CC FE 22 JAN-1999, GENE 1999071
 CC XX
 CC PR 31 JAN 1999, EMBL 0701983
 CC XX
 CC PA (UUC) 1 UNIV JOHN HOPKINS
 CC XX
 CC P1 Gruber S, Kinzler K, Iken S, Peterson C, Vogelstein B
 CC DR WP1; 1998-437490/37.
 CC XX
 CC PT Detection of mutation in APC gene, consisting T to A transversion
 CC at nucleotide 1990, useful for predicting predisposition to
 CC colorectal cancer
 CC PT
 CC XX
 CC PS Example 3; Page 11; 23pp; English.
 CC XX
 CC CC This oligonucleotide is specific for a mutant APC gene sequence and
 CC is used in the mutation analyses of the APC gene. This is used to
 CC identify the status of the inheritance of detecting a mutation in APC
 CC gene. The method uses an allele-specific nucleic acid probe which
 CC comprises a nucleic acid sequence of a region of a human mutant APC or
 CC its orthologous equivalent, where the region contains a T to A
 CC transversion at nucleotide 1990. The method is used for identifying the
 CC presence in a proband of a mutation in APC which is associated with a
 CC family history of colorectal cancer (CRC) especially among Ashkenazi
 CC Jews.
 CC CC
 CC Sequence 25 BP; 18 A; 1 C; 4 G; 2 T; 0 other;
 CC XX
 CC Query Match 54.4%; Score 13.6; DB 19; Length 25;
 CC Best Local Similarity 80.0%; Prod. No. 1.9e+04;
 CC Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC 1 TTTCTTTTATGTCGTCAT 20
 CC |||||
 CC 21 TTTCTTTTATGTCGTCAT 2
 CC
 CC DB

CC
 CC RESULT 35
 CC AAC6095
 CC ID AAC6095 standard; DNA; 25 BP.
 CC XX
 CC AC AAC6095;
 CC XX
 CC DT 26 FEB 2001 (first entry)
 CC XX
 CC DE 168 ntRNA gene 168 primer flou.
 CC XX
 CC KW DNA sequence analysis, sequencing, protein sequence, protein structure,
 CC gene typing, organ donation, bacteria identification, 16S rRNA; HLA;
 CC human leukocyte antigen, PCR primer, ss.
 CC XX
 CC OS Homo sapiens.
 CC XX
 CC PN WO200007099 AC.
 CC XX
 CC PD 02-NOV-2000.
 CC XX
 CC PR 20-APR-2000; 2000WO-BP0636.
 CC XX
 CC PR 26-APR-1999; 99EP 0303215.
 CC XX
 CC PA (AMSH) AMERSHAM PHARMACIA BIOTECH AB.
 CC XX
 CC P1 Ulfendahl P, Wang K;
 CC DR WP1; 2000-6796/1/66.
 CC XX
 CC PT Identifying extendible primers for use in identification, or
 CC PT classification of a nucleic acid of an organism, allele of gene such as
 CC PT class 1/2 HLA-sequences identifying all possible nucleotide sequences
 CC PT of specific length
 CC XX
 CC FE Claim 14, Page 45, 66p, English.
 CC XX
 CC CC The present invention provides a method for identifying a set of
 CC extendible primers which can be used in the identification, typing and
 CC classification of genes. This can then be used to predict protein
 CC sequence and structure, in organ donation to match the organ with the
 CC recipient, and to identify bacteria in a sample. The method can be used to
 CC type the human leukocyte antigen genes (HLA) and 16S rRNA genes in
 CC particular.
 CC CC
 CC Sequence 25 BP; 18 A; 1 C; 4 G; 2 T; 0 other;
 CC XX
 CC Query Match 54.4%; Score 13.6; DB 21; Length 25;
 CC Best Local Similarity 80.0%; Prod. No. 1.9e+04;
 CC Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 CC
 CC 1 TTTCTTTTATGTCGTCAT 20
 CC |||||
 CC 5 TTTCTTTTATGTCGTCAT 24
 CC
 CC RESULT 36
 CC AAC6133
 CC ID AAC6133 standard; DNA; 25 BP.
 CC XX
 CC AC AAC6133;
 CC XX
 CC DT 26 FEB 2001 (first entry)
 CC XX
 CC DE 168 ntRNA gene FCB primer #100.
 CC XX
 CC KW DNA sequence analysis, sequencing, protein sequence, protein structure,
 CC gene typing, organ donation, bacteria identification, 16S rRNA; HLA;
 CC human leukocyte antigen, PCR primer, ss.
 CC XX
 CC OS Homo sapiens.


```

OS Synthetic.
XX
XX MO9429486-A.
XX
XX 22-DEC-1994.
XX
XX
XX 15-JUN-1994; 94WO-US06810.
XX
XX 15-JUN-1994; 94US-6078471.
XX
XX 07-SEP-1993; 94US-0117952.
XX
XX (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
XX Evans GA, Smith MW.
XX
XX WPI; 1996-016508/05.
XX
XX Sequencing complex genomes, present as fragments in a cosmid
XX library, by following an specific nucleotide of each clone
XX then correlating with spatial relationship of cosmid, esp. for
XX mammalian chromosomes.
XX
XX Example 4; Page 62; 128pp; English.
XX
XX Sequences were determined from the ends of chromosome 11-specific
XX cosmids by automated sequencing without intermediate subcloning.
XX
XX A sample of 371 DNA sequence fragments were determined and of
XX these, 277 were suitable for STS primer identification by computer
XX analysis (using the "primer" program available from E. Landier, MIT).
XX The STSs and cosmids were mapped by in situ hybridisation, somatic
XX cell hybrid analysis or both. Using this method, 370 STSs specific
XX for human chromosome 11 were generated and most of them were
XX regionally mapped. This procedure illustrates a novel method for
XX sequencing complex genomes, designated "sequence sampling mapping".
XX The sequence sampling mapping method is useful for the completion of
XX high density sequence-based maps, and ultimately, for the complete
XX sequencing of genomic DNA directly from cosmid clones.
XX See AAO82001-Q82706 for STS primers.
XX
XX Sequence 22 BP; 14 A, 6 C, 1 G, 1 T, 0 other.
XX
XX Query Match 54.4%; Score 13.6; DB 16; Length 22;
XX Best local similarity 80.0%; Field No. 1; 4;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
XX
XX 5 TTTTATATGCTGCTGCTG 24
XX 22 TTTTATGCTGCTGCTG 3
XX
XX
XX RESULT 12
XX AAT15885/c
XX ID AAT15885 standard; DNA: 24 BP.
XX
XX AAT15885;
XX
XX 14 MAY-1996 (first entry)
XX
XX CD44 gene PCR primer Spt
XX
XX (CD44) exon 3, forward, nonplasmid, metastasis, bladder cancer,
XX probe, diagnosis, polymerase chain reaction, PCR, primer; ss.
XX
XX Synthetic.
XX
XX MO9603527-A2.
XX
XX 08 FEB-1996.
XX
XX 21-JUN-1994; 95WO-GH01741.
XX
XX 16 MAY-1995; 95GB-606086.
XX
XX 21-JUN-1994; 94GB-0014704

```

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PR 17 OCT-1994; 94GB-0028878.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX
XX Matsumura Y, Tatin D;
XX
XX WPI; 1996-11/068/12.
XX
XX Probes for mammalian CD44 gene, exon 3 and exon 9a sequences
XX isolated from tumour cells, used for the diagnosis of metastasis
XX
XX Disclosure, Page 16; 27pp; English.
XX
XX Primers Spt1 (AAT15885) and Spt2 (AAT15886) were used to amplify DNA
XX derived from bladder carcinoma F119 cells, normal bladder tissue,
XX bladder cancer tissue, normal urinary cell sediment, and urine
XX cell sediment. The products were used in Southern hybridizations
XX using probes for exon 3, exon 9a, and exon 9b (AAT15884, AAT15885,
XX exon 7 and exon 15 of the CD44 gene.
XX
XX Sequence 24 BP; 9 A, 7 C, 6 G, 2 T, 0 other.
XX
XX Query Match 54.4%; Score 13.6; DB 17; Length 24;
XX Best local similarity 80.0%; Field No. 1; 4;
XX Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
XX
XX 4 TTTTATATGCTGCTGCTG 25
XX 24 TTTTATGCTGCTGCTGCTG 5
XX
XX RESULT 13
XX AAV43886/c
XX ID AAV43886 standard; DNA: 24 BP.
XX
XX AAV43886;
XX
XX 26-OCT-1998 (first entry)
XX
XX APC wild-type gene specific oligonucleotide.
XX
XX APC (adenomatous polyposis coli) gene; PCR, miscense mutation, Adenomatous polyps
XX mutation analysis (hybridisation); ss.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX MO9833940-A1.
XX
XX 06-AUG-1998.
XX
XX 21-JAN-1998; 98WO-US00961.
XX
XX 31-JAN-1997; 97US-0791883.
XX
XX (UNC) UNIV JOHNS HOPKINS.
XX
XX Gruber S, Kinzler K, Laken S, Petersen G, Vogelstein B;
XX
XX WPI; 1998-437490/37.
XX
XX Detection of mutation in APC gene, consisting of a 1.5 kb region
XX at nucleotide 1929, useful for predicting predisposition to
XX colorectal cancer
XX
XX Example 3; Page 11; 23pp; English.
XX
XX This oligonucleotide is specific for the wild-type APC gene sequence and
XX is used in the mutation analyses of the APC gene. This is used to
XX identify the method of the invention of detecting a mutation in APC
XX gene. The method uses an allele-specific oligonucleotide probe which
XX comprises a nucleic acid sequence of a region of a human APC gene.

```

QY 3 TTTTTCATGTCCTGT 19
 ||||| |||||
 DB 22 TTTTATATGTCCTGT 6

RESULT 29
 AA130260/2
 ID AA130260 standard; DNA; 31 BP.
 XX
 AC AA130260;
 XX
 XX 18-OCT-2001 (first entry)
 XX
 XX Human single nucleotide polymorphism (SNP) data.
 XX
 XX Human, sequence, genotype, disease, forensic, paternity testing,
 XX single nucleotide polymorphism, SNP, etc.
 XX
 CS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Variation /tag=a
 FT /replace(16,C)
 FT /standard_name "single nucleotide polymorphism"
 FT
 XX MO200166800-A2.
 XX
 XX 13-SEP-2001.
 XX
 XX
 XX 07-MAR-2001; 2001WO-0507269.
 XX
 XX 07-MAR-2000; 2000MC-0194791
 XX 22-MAY-2000; 2000MP-0194791
 XX
 PA (MED) WHITEHEAD INST BIOMEDICAL RES.
 PI Cargill M. Ireland et al. (author)
 XX
 XX WPI; 2001-522952/57.
 XX
 XX Nucleic acid sequences from the human genome which include single
 XX sites, useful in methods for predicting the presence, absence or
 XX severity of a particular form of a disease or disorder.
 XX associated with a particular genotype
 XX
 XX Claim 1; Page 75; 14pp; English.
 XX
 CC The invention relates to the identification of nucleic acid sequences
 CC (AA129513) associated with the human genome which include single
 CC sites, useful in methods for predicting the presence, absence or
 CC severity of a particular form of a disease or disorder.
 CC (CNF) in these genes discovered. The method is useful for predicting the
 CC presence, absence or severity of a particular phenotype in the human
 CC (diabetes) associated with a particular genotype. The method is also
 CC containing the polymorphic sites may be useful in forensic and paternity
 XX testing.
 XX
 XX Sequence 31 BP; 15 A; 8 C; 3 G; 5 T; 0 other;
 XX

Query Map 1 55 31. Score 13.5. Length 25.
 Best Local Similarity 22.08. E-Val. 1.0e-04.
 Matches 15. Conserved 0. Mismatch 0. Indels 0. Gap 0.

QY 1 TTTTTCATGTCCTGTGTA 25
 ||||| ||||| |||||
 DB 27 TTTTATATGTCCTGTGTA 3

RESULT 30
 AAD12815
 ID AAD12815 standard; DNA; 22 BP
 XX

AC AAD12815;
 XX
 XX 16-OCT-2001 (first entry)
 XX
 XX Solanum tuberosum gsm1 promoter (539 to +48) reverse PCR primer.
 XX
 XX Solanum tuberosum gsm1 promoter (539 to +48) reverse PCR primer.
 XX
 XX Hypersensitive response elicitor, promoter, transgenic plant, infection,
 XX gene therapy, and loss, analysis, factor, PCR primer, etc.
 XX
 XX Solanum tuberosum.
 XX
 XX WO200155347-A1.
 XX
 XX 02-AUG-2001.
 XX
 XX 26-JAN-2001; 2001WO-US02579.
 XX
 XX 26-JAN-2001; 2000US-0179565.
 XX
 XX (COPR) COPRHLR R&S FOUND INC.
 XX
 XX Best SW. Bauer DM;
 XX
 XX WPI; 2001-499791/53.
 XX
 XX
 XX New chimeric gene, useful for controlling plant-pathogenic fungi and
 XX producing transgenic resistant transgenic plants, comprising first DNA
 XX encoding hypersensitive response elicitor, promoter and regulatory
 XX region.
 XX
 XX Example 1; Page 33; 72pp; English.
 XX
 XX The invention relates to a chimeric gene that includes a first DNA
 XX molecule encoding a hypersensitive response elicitor protein or
 XX polypeptide, preferably linked to the first DNA molecule
 XX encoding transcription of the first DNA molecule in response to
 XX activation of the first DNA molecule and a regulatory region
 XX operably linked to the first DNA molecule. The second DNA molecule
 XX to a transgenic plant resistant to disease resulting from complete
 XX infection, the transgenic plant including the chimeric gene, wherein
 XX the promoter induces transcription of the first DNA molecule in
 XX response to infection of the plant by a pathogen. The chimeric gene
 XX is used in gene therapy. The chimeric gene is useful as an effective
 XX resistance gene of controlling plant pathogenic fungi, particularly
 XX fungi, which are responsible for plant diseases and is also useful
 XX for producing transgenic plants of the invention. The present sequence
 XX is a PCR primer used to amplify Solanum tuberosum gsm1 promoter region
 XX (539 to +48).
 XX
 XX Solanum tuberosum gsm1; 4 A; 0 C; 3 G; 15 T; 0 other;
 XX

Query Map 1 55 31. Score 13.5. Length 25.
 Best Local Similarity 22.08. E-Val. 1.0e-04.
 Matches 15. Conserved 0. Mismatch 0. Indels 0. Gap 0.

QY 1 TTTTTCATGTCCTGTGTA 23
 ||||| ||||| |||||
 DB 8 TTTTATATGTCCTGTGTA 24

RESULT 31
 AAG92023/C
 ID AAG92023 standard; DNA; 22 BP.
 XX
 XX AAG92023;
 XX
 XX 30-APR-1994 (first entry)
 XX
 XX Chromosome 11 (human) STS primer c11g-563-b1.
 XX
 XX Sequence sampled method; genomic analysis, copy number analysis,
 XX genetic library, and gene expression analysis, PCR primer, etc.
 XX


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XX PA 1AECM: AECMICA INC.
XX PI Zhang J.
XX DR WPI: 2002-479509/51.
XX PT New human kidney and liver tissue (KTM1) is used to
XX PT nucleic acids encoding the protein useful for treating subjects having
XX PT defects in KTM1 which can manifest as disorder of the kidney, liver or
XX PT disorder of e.g., liver or bone.
XX PS Example 2, Page 225; 145pp; English.
XX CC The invention relates to a novel polypeptide and a method of using the
XX CC KTM1 (kidney tissue) polypeptide. The polypeptide may have a use in gene
XX CC invention has cytoprotective activity. The polypeptide may have a use in gene
XX CC therapy. The KTM1 nucleic acids may be used to identify, treat or
XX CC monitor a disease caused by altered expression of human KTM1.
XX CC Compositions comprising the nucleic acids, it is used for the
XX CC used to treat subjects having defects in KTM1 which can manifest as
XX CC disorder of the kidney, as well as a disorder of liver, bone marrow, brain,
XX CC heart, lung, kidney, colon, skeletal muscle, testis, uterus and placenta
XX CC function. The sequence represents a probe used in the invention to
XX CC search for a KTM1 gene.
XX CC Sequence 25 BF, 6 A; 5 G; 3 T; 0 other;
XX CC
XX CC Query Match: 59.23; Score 14.5; EB 24; Length 25;
XX CC Best Local Similarity: 89.94; Prod No. 619403;
XX CC Matched: 10; Conserved: 0; Mismatch: 0; Indels: 0; Type:
XX CC
XX CC 1 TTTCTTTCTGATGTCGTCG 19
XX CC 1 TTTCTTTCTGATGTCGTCG 19
XX CC
XX CC RESULT 11
XX CC AA33736/C
XX CC ID AA33736 standard; DNA; 24 BP.
XX CC
XX CC AA33736;
XX CC
XX CC 25-DEC-1999 (first entry)
XX CC
XX CC DNA tandem nucleotide repeat locus FOR primer SEQ ID NO 25.
XX CC
XX CC DNA tandem nucleotide repeat locus; human; DMP allele; genetic mapping;
XX CC genetic identity; detection; clinical identification; paternity testing;
XX CC PCR primer; GC.
XX CC
XX CC Synthesis:
XX CC Homo sapiens.
XX CC
XX CC WO914375-A2.
XX CC
XX CC 25-MAR-1999.
XX CC
XX CC 19-SEP-1999; 99007519878.
XX CC
XX CC 19-SEP-1997; 9705-0059415.
XX CC
XX CC (GENE-) GENETRACE SYSTEMS INC.
XX CC
XX CC Becker CA, Rurler JM, Li J, Montforte J.
XX CC
XX CC WPI: 1999-103554/19.
XX CC
XX CC Analysis of DNA tandem nucleotide repeat alleles by extending a
XX CC primer with a primer containing a nucleotide sequence which
XX CC Claim 99; Page 26; 1997; English
XX CC

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XX CC This sequence represents a PCR primer for a DNA tandem nucleotide repeat
XX CC (DMP) locus that can be used in the method of the invention.
XX CC The method is for analysing DMP alleles in a target nucleic acid,
XX CC and comprises extending the target nucleic acid using primers
XX CC complementary to sequences flanking the repeat and analysing the
XX CC spectrum. The primers and methods can be used for genetic
XX CC identity detection including forensic identification and paternity
XX CC testing as well as genetic mapping. The use of such spectrum for
XX CC characterizing DMPs provides for high speed of analysis in few seconds
XX CC per sample and accurate direct read measurements.
XX CC
XX CC Sequence 24 BF, 13 A; 5 G; 2 C; 4 T; 0 other;
XX CC
XX CC Query Match: 59.44; Score 14.5; EB 20; Length 24;
XX CC Best Local Similarity: 89.94; Prod No. 619403;
XX CC Matched: 17; Conserved: 0; Mismatch: 4; Indels: 0; Type:
XX CC
XX CC 1 TTTCTTTCTGATGTCGTCG 25
XX CC 1 TTTCTTTCTGATGTCGTCG 1
XX CC
XX CC RESULT 12
XX CC AA330252
XX CC ID AA330252 standard; DNA; 31 BP.
XX CC
XX CC AA330252;
XX CC
XX CC 19-DEC-2001 (first entry)
XX CC
XX CC Homo sapiens.
XX CC
XX CC Human, sequence, genotype, disease, forensic, paternity testing;
XX CC single nucleotide polymorphism; SNP; ss.
XX CC
XX CC Homo sapiens.
XX CC
XX CC Key:
XX CC Location/Qualifiers
XX CC FT Variation
XX CC FT /tag= a
XX CC FT /standard_name= "single nucleotide polymorphism"
XX CC
XX CC WO9016690-A2.
XX CC
XX CC 13-SEP-2001.
XX CC
XX CC 07-MAR-2001; 200100-030/268.
XX CC
XX CC of XNA, 400000-0100/510.
XX CC 22 MAR 2000; 200000-0006129.
XX CC
XX CC (WHEAT) WHITEHEAD INST BIOMEDICAL RES.
XX CC
XX CC Cargill M, Ireland US, Lander ES.
XX CC
XX CC WPI: 2001-522952/57.
XX CC
XX CC Claim 1; Page 74; 145pp; English.
XX CC
XX CC The invention relates to the identification of nucleic acid molecules
XX CC (AA330252-AA330252) from the human genome which include polymorphic sites
XX CC which can predispose individuals to disease. Nucleic acids that a subset
XX CC of individuals were resequenced and single nucleotide polymorphisms
XX CC (SNPs) in these genes were discovered. The method is useful for predicting the
XX CC frequency, frequency, and severity of a particular phenotype or disorder (e.g., diabetes)
XX CC associated with a particular genotype. The nucleic acids
XX CC containing the polymorphic sites may be used in forensics and paternity
XX CC testing.
XX CC

```


[illegible][illegible]

[illegible]

375	11.6	45.4	25	22	AAAG2721	Primer A H4s used	C	442	11.4	45.6	20	22	AAAG2942	Human PVLG11, 100
376	11.6	45.4	24	22	AAH48161	Purified lysate 13	C	443	11.4	45.6	20	24	AAAG2925	Mouse cAMPAR1
377	11.6	46.4	24	24	AAH19148	Human CCR5 promoter	C	444	11.4	45.6	21	13	AAAG34394	Downstream primer for p3
378	11.6	46.4	25	24	AAH46940	Box 2 antisense of	C	445	11.4	45.6	21	16	AAAG75845	Prostate 1 transcript
379	11.6	46.4	25	13	AAAG34345	Upstream PCR primer	C	452	11.4	45.6	21	19	AAAG67317	Prostate 1b transcript
380	11.6	46.4	25	21	AAAG27008	HLA EBI1 gene PCR	C	453	11.4	45.6	21	24	AAAG29746	Cytokeratin 14c
381	11.6	46.4	25	21	AAAG27201	HLA DPA1 gene PCR	C	454	11.4	45.6	21	24	AAH44026	Human chromosome 1
382	11.6	46.4	25	21	AAAG28412	HLA DPA2 gene PCR	C	455	11.4	45.6	22	22	AAAG58924	Human chromosome 1
383	11.6	46.4	25	21	AAAG28549	HLA HLA-B gene PCR	C	456	11.4	45.6	22	22	AAAG67574	Human chromosome 1
384	11.6	46.4	25	21	AAAG29545	HLA HLA-B gene PCR	C	457	11.4	45.6	22	24	AAAG75644	Human chromosome 1
385	11.6	46.4	25	21	AAAG29589	HLA HLA-C gene PCR	C	458	11.4	45.6	24	21	AAAG75879	Human chromosome 1
386	11.6	46.4	25	21	AAAG29594	HLA HLA-C gene PCR	C	459	11.4	45.6	24	22	AAAG4817	Human chromosome 1
387	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	460	11.4	45.6	24	24	AAAG55598	Human chromosome 1
388	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	461	11.4	45.6	24	24	AAAG55598	Human chromosome 1
389	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	462	11.4	45.6	24	24	AAAG55598	Human chromosome 1
390	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	463	11.4	45.6	24	24	AAAG55598	Human chromosome 1
391	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	464	11.4	45.6	24	24	AAAG55598	Human chromosome 1
392	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	465	11.4	45.6	24	24	AAAG55598	Human chromosome 1
393	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	466	11.4	45.6	24	24	AAAG55598	Human chromosome 1
394	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	467	11.4	45.6	25	21	AAAG67324	Human chromosome 1
395	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	468	11.4	45.6	25	21	AAAG67324	Human chromosome 1
396	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	469	11.4	45.6	25	21	AAAG67324	Human chromosome 1
397	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	470	11.4	45.6	25	21	AAAG67324	Human chromosome 1
398	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	471	11.4	45.6	25	21	AAAG67324	Human chromosome 1
399	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	472	11.4	45.6	25	21	AAAG67324	Human chromosome 1
400	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	473	11.4	45.6	25	21	AAAG67324	Human chromosome 1
401	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	474	11.4	45.6	25	21	AAAG67324	Human chromosome 1
402	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	475	11.4	45.6	25	21	AAAG67324	Human chromosome 1
403	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	476	11.4	45.6	25	21	AAAG67324	Human chromosome 1
404	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR	C	477	11.4	45.6	25	21	AAAG67324	Human chromosome 1
405	11.6	46.4	25	21	AAAG29634	HLA EBI1 gene PCR</								



DN 23 TTTCTTTCTGTGATGTGTG 1

RESULT 40
AR170667/2 AR170667 31 bp DNA linear PAT 17 DEC-2001

LOCUS Sequence 101 from Patient US 6291664.
DEFINITION AR170667
ACCESSION AR170667
VERSION AR170667.1 GI:17908626
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 31)
AUTHORS Pavlakis G.N. and Folber P.K.
TITLE Method of determining inheritance/identity regions of mtDNA
JOURNAL Patient: US 6291664-A 101 18 SEP 2001;
Location/Qualifiers
FEATURES
Source 1..31
/organism="unknown"

BASE COUNT 17 a 7 c 3 g 4 t
ORIGIN

Query Match 93.6%, Score 13.4; DP 6; Length 31;
Best Local Similarity 73.9%; P-adj. No. 2.6e+05;
Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2 TTTCTTTCTGTGATGTGTG 24
23 TTTCTTTCTGTGATGTGTG 1

Search completed: July 21, 2003, 14:35:22
Job time : 265.581 secs


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RESULT 35
LOCUS       177011
DEFINITION  24 Jan 97: 30 bp. DNA
ACCESSION   177011
VERSION     177011
KEYWORDS    177011
SOURCE      Unknown
ORGANISM    Unknown
REFERENCE   1 (bases 1 to 30)
AUTHOR(s)  Shattuck-Schneider, D.M., Seward, J., Durocher, F., Emi, M. and Nakamura, Y.
TITLE      Linked breast and ovarian cancer susceptibility gene
JOURNAL    Patent: US 5693473-A 71 02-DEC-1997;
FEATURES    Location/Qualifiers
             source          1..30
             BASE COUNT     5 a 6 c 4 g 15 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 30
Best Local Similarity 20.0%, Fred. No. 2.6e+05;
Matches 16/ Conservative 0/ Mismatches 4/ Indels 0/ Gaps 0/
CY          1 TTTTTCATGATGCTT 20
           1 ||||| ||||| |||||
DB          8 TTTTTCATGATGCTT 27

RESULT 36
LOCUS       181006
DEFINITION  Sequence 71 from Patent US 5693473.
ACCESSION   181006
VERSION     181006
KEYWORDS    181006
SOURCE      Unknown
ORGANISM    Unknown
REFERENCE   1 (bases 1 to 30)
AUTHOR(s)  Shattuck-Schneider, D.M., Seward, J., Durocher, F., Emi, M. and Nakamura, Y.
TITLE      Linked breast and ovarian cancer susceptibility gene
JOURNAL    Patent: US 5693473-A 71 02-DEC-1997;
FEATURES    Location/Qualifiers
             source          1..30
             BASE COUNT     5 a 6 c 4 g 15 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 30
Best Local Similarity 20.0%, Fred. No. 2.6e+05;
Matches 16/ Conservative 0/ Mismatches 4/ Indels 0/ Gaps 0/
CY          1 TTTTTCATGATGCTT 20
           1 ||||| ||||| |||||
DB          8 TTTTTCATGATGCTT 27

RESULT 37
LOCUS       181102
DEFINITION  Sequence 71 from Patent US 5710991.
ACCESSION   181102
VERSION     181102
KEYWORDS    181102
SOURCE      Unknown
ORGANISM    Unknown
REFERENCE   1 (bases 1 to 30)
AUTHOR(s)  Skolnick, M.H., Goldberg, P.F., Milvi, Y., Swenson, J., Kaob, A., Harshman, P.F., Shattuck-Schneider, D.M., Tye, J.D., S.V., Miesman, P.W.
TITLE      Linked breast and ovarian cancer susceptibility gene
JOURNAL    Patent: US 5710991-A 71 02-DEC-1997;
FEATURES    Location/Qualifiers
             source          1..30
             BASE COUNT     5 a 6 c 4 g 15 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 30
Best Local Similarity 20.0%, Fred. No. 2.6e+05;
Matches 16/ Conservative 0/ Mismatches 4/ Indels 0/ Gaps 0/
CY          1 TTTTTCATGATGCTT 20
           1 ||||| ||||| |||||
DB          8 TTTTTCATGATGCTT 27

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TITLE      and Futreal, P. Andrew.
JOURNAL    17q linked breast and ovarian cancer susceptibility gene
PATENT     Patent: US 5710991-A 71 02-DEC-1997;
FEATURES    Location/Qualifiers
             source          1..30
             BASE COUNT     5 a 6 c 4 g 15 t
ORIGIN
Query Match 54.4% Score 13.6 DB 6 Length 30
Best Local Similarity 20.0%, Fred. No. 2.6e+05;
Matches 16/ Conservative 0/ Mismatches 4/ Indels 0/ Gaps 0/
CY          1 TTTTTCATGATGCTT 20
           1 ||||| ||||| |||||
DB          8 TTTTTCATGATGCTT 27

RESULT 38
LOCUS       AP079777/c
DEFINITION  Sequence 101 from Patent US 5685726.
ACCESSION   AP079777
VERSION     AP079777
KEYWORDS    AP079777
SOURCE      Unknown
ORGANISM    Unknown
REFERENCE   1 (bases 1 to 31)
AUTHOR(s)  Pavlakis, G.N. and Felber, P.K.
TITLE      Method of eliminating inhibitory/instability regions of DNA
JOURNAL    Patent: US 5685726-A 70 12-001-1999;
FEATURES    Location/Qualifiers
             source          1..31
             BASE COUNT     17 a 7 c 3 g 4 t
ORIGIN
Query Match 53.6% Score 13.4 DB 6 Length 31
Best Local Similarity 70.9%, Fred. No. 2.6e+05;
Matches 17/ Conservative 0/ Mismatches 6/ Indels 0/ Gaps 0/
CY          7 TTTTTCATGATGCTTGGT 24
           7 ||||| ||||| |||||
DB          23 TTTTTCATGATGCTTGGT 24

RESULT 39
LOCUS       AP081307/c
DEFINITION  Sequence 103 from Patent US 5972596.
ACCESSION   AP081307
VERSION     AP081307
KEYWORDS    AP081307
SOURCE      Unknown
ORGANISM    Unknown
REFERENCE   1 (bases 1 to 31)
AUTHOR(s)  Pavlakis, G.N. and Felber, P.K.
TITLE      Nucleic acid constructs containing HIV genes with mutation inhibitory/instability regions and methods of using same
JOURNAL    Patent: US 5972596-A 70 12-001-1999;
FEATURES    Location/Qualifiers
             source          1..31
             BASE COUNT     17 a 7 c 3 g 4 t
ORIGIN
Query Match 53.6% Score 13.4 DB 6 Length 31
Best Local Similarity 70.9%, Fred. No. 2.6e+05;
Matches 17/ Conservative 0/ Mismatches 6/ Indels 0/ Gaps 0/
CY          2 TTTTTCATGATGCTTGGT 24

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ORIGIN

Query Match 54.4% Score 13.6 DB 6 Length 22
 Best Local Similarity 89.2% Fred. No. 186055
 Matches 15 Conservative 0 Mismatches 1 Indels 0 Gaps 0

Db 1 TTTCTTTCTATGCT 17
 9 TTTCTTTCTATGCT 25

RESULT 26
 LOCUS AX476119 25 bp DNA linear PAT 24 NOV 2002
 DEFINITION Sequence 1340 from Patent WO024750.
 ACCESSION AX476119
 VERSION AX476119.1 GI:22216404
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Carnivoria; Homnidae; Homo

REFERENCE 1
 AUTHORS Zhang, J.
 TITLE Human vitronectin cytochrome c membrane protein 1
 JOURNAL Patent: WO 024750 A 1940 24 MAR 2002
 AEMICAL, INC. (US)
 LOCATION/Qualifiers
 1..25
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 6 a 6 c 5 g 8 t
 ORIGIN

Query Match 54.4% Score 13.6 DB 6 Length 22
 Best Local Similarity 89.2% Fred. No. 186055
 Matches 15 Conservative 0 Mismatches 1 Indels 0 Gaps 0

Db 2 TTTCTTTCTATGCT 18
 1 TTTCTTTCTATGCT 17

RESULT 27
 LOCUS AR066675.1 18 bp DNA linear PAT 20 SEP 1999
 DEFINITION Sequence 21 from Patent US 5851760.
 ACCESSION AR066675
 VERSION AR066675.1 GI:5937837
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Carnivoria; Homnidae; Homo

REFERENCE 1 (bases 1 to 22)
 AUTHORS Evans, C.A. and Smith, M.W.
 TITLE Method for generation of sequence sampled maps of complex genomes
 JOURNAL Patent: US 5851760-A 23 22-DEC-1998
 LOCATION/Qualifiers
 1..22
 /organism="Unknown"

BASE COUNT 14 a 6 c 1 g 1 t
 ORIGIN

Query Match 54.4% Score 13.6 DB 6 Length 22
 Best Local Similarity 89.2% Fred. No. 186055
 Matches 15 Conservative 0 Mismatches 1 Indels 0 Gaps 0

Db 22 TTTCTTTCTATGCT 3

RESULT 28

AA8478/c

LOCUS AA8478 24 bp DNA linear PAT 24 MAR 1999
 DEFINITION Sequence 17 from Patent WO000707.
 ACCESSION AA8478
 VERSION AA8478.1 GI:200267
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Carnivoria; Homnidae; Homo

REFERENCE 1 (bases 1 to 24)
 AUTHORS Tatin, D. and Matsumura, Y.
 TITLE DIAGNOSTIC METHOD AND PCR REAGENT FOR DETECTION OF
 JOURNAL Patent: WO 000572/A 1 02-SEP-1999
 1505 1505-0005 (GB)
 LOCATION/Qualifiers
 1..24
 /organism="unidentified"
 /db_xref="taxon:9606"

BASE COUNT 9 a 7 c 6 g 2 t
 ORIGIN

Query Match 54.4% Score 13.6 DB 6 Length 24
 Best Local Similarity 89.0% Fred. No. 202005
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

Db 24 TTTCTTTCTATGCT 25
 24 TTTCTTTCTATGCT 25

RESULT 29
 LOCUS AX042958 25 bp DNA linear PAT 24 NOV 2002
 DEFINITION Sequence 524 from Patent WO065088.
 ACCESSION AX042958
 VERSION AX042958.1 GI:1194566
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Carnivoria; Homnidae; Homo

REFERENCE 1 (bases 1 to 25)
 AUTHORS Ullendahl, P. J. and Wang, R. C.
 TITLE Primers for identifying typing of clonally derived nucleic acids
 JOURNAL Patent: WO 065088 A 524 02 NOV 2002
 AEMICAL, INC. (US)
 LOCATION/Qualifiers
 1..25
 /organism="synthetic construct"
 /db_xref="taxon:9606"

BASE COUNT 3 a 1 c 3 g 19 t
 ORIGIN

Query Match 54.4% Score 13.6 DB 6 Length 24
 Best Local Similarity 89.0% Fred. No. 202005
 Matches 16 Conservative 0 Mismatches 4 Indels 0 Gaps 0

Db 5 TTTCTTTCTATGCT 24
 5 TTTCTTTCTATGCT 24

RESULT 30
 LOCUS AX042956 25 bp DNA linear PAT 24 NOV 2002
 DEFINITION Sequence 524 from Patent WO065088.
 ACCESSION AX042956
 VERSION AX042956.1 GI:1194564
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Carnivoria; Homnidae; Homo

REFERENCE 1 (bases 1 to 25)

AX476133 17 bp DNA Human PAT 12 AUG 2002

LOCUS AX476133 174 bp 17 bp 17 bp
DEFINITION Human
ACCESSION AX476133
VERSION AX476133.1
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
REFERENCE
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL
JOURNAL
Aeomica, Inc. (US)

FEATURES
SOURCE
1..17
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 1 a 4 c 3 g 9 t
ORIGIN

Query Match 55.2% Score 13.87 E-6 Length 17
Best Local Similarity 55.2% E-6 Length 17
Matches 15, Conservation 2, Mismatches 2, Indels 0, Gaps 0

QY 1 TTCTCTTCATATGCT 17
|||||
1 TTCTCTTCATATGCT 17

Db 1 TTCTCTTCATATGCT 17

RESULT 22
AX476134 17 bp DNA Human PAT 12 AUG 2002
LOCUS AX476134 174 bp 17 bp 17 bp
DEFINITION Human
ACCESSION AX476134
VERSION AX476134.1
KEYWORDS
SOURCE human
ORGANISM Homo sapiens
REFERENCE
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL
JOURNAL
Aeomica, Inc. (US)

FEATURES
SOURCE
1..17
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 1 a 4 c 4 g 8 t
ORIGIN

Query Match 55.2% Score 13.87 E-6 Length 17
Best Local Similarity 55.2% E-6 Length 17
Matches 15, Conservation 2, Mismatches 2, Indels 0, Gaps 0

QY 2 TTCTCTTCATATGCT 18
|||||
1 TTCTCTTCATATGCT 17

Db 1 TTCTCTTCATATGCT 17

REFERENCE 1 (bases 1 to 20)
AUTHORS Lemstra, C.J., and Vickers, T.A.
TITLE Expression of Rb protein
JOURNAL
JOURNAL
location/Qualifiers
1..20
/organism="unknown"
BASE COUNT 11 a 3 c 5 g 1 t
ORIGIN

Query Match 55.2% Score 13.87 E-6 Length 20
Best Local Similarity 55.2% E-6 Length 20
Matches 17, Conservation 2, Mismatches 2, Indels 0, Gaps 0

QY 1 TTCTCTTCATATGCT 18
|||||
1 TTCTCTTCATATGCT 17

Db 1 TTCTCTTCATATGCT 17

RESULT 24
AX043229 25 bp DNA Human PAT 12 AUG 2002
LOCUS AX043229 174 bp 25 bp 25 bp
DEFINITION Human
ACCESSION AX043229
VERSION AX043229.1
KEYWORDS
SOURCE
ORGANISM
synthetic construct.
synthetic construct.
artificial sequences.
REFERENCE
AUTHORS Ulfendahl, P.C. and Wong, K.C.
TITLE Primers for identifying typing of classifying nucleic acids
JOURNAL
JOURNAL
Aeomica, Inc. (US)

FEATURES
SOURCE
1..25
/organism="synthetic construct"
/db_xref="taxon:3630"
/note="CDT1 Heteroduplex Filter Sequences"

BASE COUNT 3 a 3 c 4 g 15 t
ORIGIN

Query Match 55.2% Score 13.87 E-6 Length 25
Best Local Similarity 55.2% E-6 Length 25
Matches 15, Conservation 2, Mismatches 2, Indels 0, Gaps 0

QY 1 TTCTCTTCATATGCT 25
|||||
1 TTCTCTTCATATGCT 17

Db 1 TTCTCTTCATATGCT 17

RESULT 25
AX476110 25 bp DNA Human PAT 12 AUG 2002
LOCUS AX476110 174 bp 25 bp 25 bp
DEFINITION Human
ACCESSION AX476110
VERSION AX476110.1
KEYWORDS
SOURCE
ORGANISM
human.
Homo sapiens
REFERENCE
AUTHORS Zhang, J.
TITLE Human kidney tumor overexpressed membrane protein 1
JOURNAL
JOURNAL
Aeomica, Inc. (US)

FEATURES
SOURCE
1..25
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 3 a 6 c 5 g 11 t
ORIGIN

AUTHORS Kanazawa, J., Goto, J., and Jeong, S. Y.
 TITLE Human sodium channel SCN12A and SCN8A
 JOURNAL J. Neurosci. 23: 1144-1150, 2003
 JAFETY STATEMENT AND IF YOU HAVE ANY COMMENTS, PLEASE CONTACT THE JOURNAL AT JN@SOCIETYFORNEUROSCIENCE.ORG

COMMENT
 OS Artificial Sequence
 PN WO 0150355-A/13
 PD 29-NOV-2001
 PR 11-JUL-2000 WO 99/40044-29
 PR 23-MAY-2000 JP 00P 152085
 P1 ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG
 PC GENE/12/00014/4/00016/18
 CC Artificial Sequence; Synthesized oligonucleotide FH key

FEATURES
 source
 1..27
 /organism="synthetic construct"
 /db_xref="taxon:32630"

BASE COUNT
 1 a 5 c 10 g 3 t

ORIGIN

Query Match
 Best Local Similarity 56.0%, Score 14, DB 6, Length 27,
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

2Y 4 CTTTCTATGAGTGTGTGTTGCA 25
 |||||
 4 CTTTCTATGAGTGTGTGTTGCA 25

Db
 4 CTTTCTATGAGTGTGTGTTGCA 25

RESULT 18
 RD004574 standard, ENA, CYN, 27 BP.

XX RD004574
 AC RD004574
 SV RD004574.1
 XX

21 08-FEB-2002 (rel. 10, created)
 27 08-FEB-2002 (rel. 10, last updated, Version 1)

XX DE Human sodium channel SCN12A and SCN8A.
 XX KW JP 03074556-1/13.
 XX OS Synthetic construct
 XX artificial sequence

XX [1]
 RN 1-27
 RA Kanazawa J, Goto J, Jeong S Y
 RT "Human sodium channel SCN12A and SCN8A"
 RL Patient number JF010/4556-1/13, 19-JAN-2001.
 RU JAFETY STATEMENT AND IF YOU HAVE ANY COMMENTS, PLEASE CONTACT THE JOURNAL AT JN@SOCIETYFORNEUROSCIENCE.ORG

XX
 CC Artificial Sequence
 CC PN JP 03074556-1/13
 CC PD 19-JAN-2001
 CC PR 11-JUL-2000 JP 000004429
 CC PR 23-MAY-2000 JP 00P 152085
 CC P1 ICHIRO KANAZAWA, JUN GOTO, SEON YONG JEONG
 CC PC GENE/12/00014/4/00016/18
 CC CC Artificial Sequence; Synthesized oligonucleotide FH key

XX
 CC KEY Location/Qualifiers
 CC FH 1..27
 CC FT source
 CC FT /organism="Artificial Sequence"

XX
 FH key Location/Qualifiers
 FH 1..27
 FH FT source
 FH FT /db_xref="taxon:32630"
 FH FT /organism="synthetic construct"

XX

Sequence 27 BP, 1 A, 5 C, 10 G, 3 T, 0 other

Query Match
 Best Local Similarity 56.0%, Score 14, DB 6, Length 27,
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

2Y 4 CTTTCTATGAGTGTGTGTTGCA 25
 |||||
 4 CTTTCTATGAGTGTGTGTTGCA 25

Db
 4 CTTTCTATGAGTGTGTGTTGCA 25

RESULT 19
 AX192016/c
 Sequence 46 from Patent WO1498501
 ACCESSION AX192016
 VERSION AX192016.1
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct,
 artificial sequences,
 1 (bases 1 to 29)
 REFERENCE
 Goto, J, S. Goto, A. D. Halperin, J. Kanazawa, and S. Y. Jeong
 Artificially synthesized enzyme and lysosomal enzyme precursor
 Patent: WO 0149850 A 46 (2001-07-2001)
 Maxygen Aps (DK)

FEATURES
 source
 1..29
 Location/Qualifiers
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Primer"

BASE COUNT
 10 a 8 c 7 g 4 t

ORIGIN

Query Match
 Best Local Similarity 77.3%, Score 14, DB 6, Length 27,
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

2Y 2 TTTTCTATGAGTGTGTGTTGCT 23
 |||||
 25 TACTCTATGAGTGTGTGTTGCT 4

Db
 25 TACTCTATGAGTGTGTGTTGCT 4

RESULT 20
 LS8015/c
 LOCUS LS8015 30 bp ENA
 REFERENCE Sequence 8 from Patent WO 97/11997
 ACCESSION LS8015
 VERSION LS8015.1
 KEYWORDS
 SOURCE
 ORGANISM
 Unknown,
 Unclassified,
 1 (bases 1 to 30)
 AUTHORS
 Nikiforov, T. and Knapp, M. R.
 TITLE Method for immobilizing nucleic acid molecules
 JOURNAL Future of Biotechnology 11: 199-200
 FEATURES
 source
 1..30
 Location/Qualifiers
 /organism="unknown"

BASE COUNT
 9 a 10 c 5 g 6 t

ORIGIN

Query Match
 Best Local Similarity 56.0%, Score 14, DB 6, Length 27,
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

2Y 2 TTTTCTATGAGTGTGTGTTGCT 23
 |||||
 25 TACTCTATGAGTGTGTGTTGCT 5

Db
 25 TACTCTATGAGTGTGTGTTGCT 5

RESULT 21

DEFINITION Sequence 1008 from Patent WO9324490.
 ACCESSION AX476117
 VERSION AX476117.1 GI:22215402
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Crustacea; Vertebrata; Eumetazoa; Mammalia; Primates; Carnivora; Hominoidea; Homo

REFERENCE
 1 Zhang, J.
 TITLE Human kidney tumor overexpressed membrane protein 1
 JOURNAL Patent: WO 9324490 A 139 28 MAR 2002
 AUTHOR Zhang, J.
 INVENTOR Zhang, J.
 APPLICANT Accutact, Inc. (US)
 LOCATION/Qualifiers location/Qualifiers

FEATURES
 source 1..25
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 5 a 5 c 5 g 5 t

ORIGIN

Query Match 59.2% Score 14.8; DB 6; Length 25;
 Best local Similarity 99.9%; Pred. No. 6.5e+04;
 Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0

CY 1 TTTCTTTTATGATGCTG 18
 |||||
 2 TTTCTTTTATGATGCTG 19

Db

RESULT 9
 LOCUS AX476118 25 bp DNA linear PAT 12 NOV 2002
 DEFINITION Sequence 1008 from Patent WO9324490.
 ACCESSION AX476118
 VERSION AX476118.1 GI:22215403
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Crustacea; Vertebrata; Eumetazoa; Mammalia; Primates; Carnivora; Hominoidea; Homo

REFERENCE
 1 Zhang, J.
 TITLE Human kidney tumor overexpressed membrane protein 1
 JOURNAL Patent: WO 9324490 A 139 28 MAR 2002
 AUTHOR Zhang, J.
 INVENTOR Zhang, J.
 APPLICANT Accutact, Inc. (US)
 LOCATION/Qualifiers location/Qualifiers

FEATURES
 source 1..25
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

BASE COUNT 5 a 5 c 5 g 5 t

ORIGIN

Query Match 59.2% Score 14.8; DB 6; Length 25;
 Best local Similarity 99.9%; Pred. No. 6.5e+04;
 Matches 16; Conservative 0; Mismatches 7; Indels 0; Gaps 0

CY 1 TTTCTTTTATGATGCTG 18
 |||||
 2 TTTCTTTTATGATGCTG 19

Db

RESULT 10
 LOCUS A11317 24 bp DNA linear PAT 03 NOV 1995
 DEFINITION Chimeric nucleotide from Patent EP0414129.
 ACCESSION A11317
 VERSION A11317.1 GI:1249339
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM artificial sequences
 1 (bases 1 to 24)
 REFERENCE
 1 (bases 1 to 24)
 AUTHORS Sripth, M. and Thomas, P.

TITLE Hybrid protein for the 16 kDa antigen from W. heterophila, Escherichia coli as host, the 38 kDa antigen and a 3 kDa protein
 JOURNAL Patent: EP 0414129 A 4 24 DEC 1992
 AUTHOR Gesslitschko, Peter
 INVENTOR Gesslitschko, Peter
 APPLICANT Biologische Forschungslab GmbH (DE)
 LOCATION/Qualifiers location/Qualifiers

FEATURES
 source 1..28
 /organism="synthetic construct"
 /db_xref="taxon:32630"

BASE COUNT 3 a 5 c 8 g 12 t

ORIGIN

Query Match 58.4% Score 14.6; DB 6; Length 24;
 Best local Similarity 81.9%; Pred. No. 7.9e+04;
 Matches 17; Conservative 0; Mismatches 4; Indels 0; Gaps 0

CY 2 TTTCTTTTATGATGCTG 22
 |||||
 2 TTTCTTTTATGATGCTG 22

Db

RESULT 11
 LOCUS AX043457 25 bp DNA linear PAT 24 NOV 2000
 DEFINITION Sequence 1023 from Patent WO965088.
 ACCESSION AX043457
 VERSION AX043457.1 GI:11342065
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM artificial construct.
 1 (bases 1 to 25)
 REFERENCE
 1 (bases 1 to 25)
 AUTHORS Hlfordahl, P. J. and Wong, K. C.
 TITLE Plasmid for identifying and cloning of differentiating nuclear acids
 JOURNAL Patent: WO 965088 A 100 24 NOV 2000
 AUTHOR Hlfordahl, P. J. and Wong, K. C.
 INVENTOR Hlfordahl, P. J. and Wong, K. C.
 APPLICANT Amer sham Pharmaceuticals (US)
 LOCATION/Qualifiers location/Qualifiers

FEATURES
 source 1..25
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="DRB145 Heterozygote Primer Sequence"

BASE COUNT 2 a 2 c 5 g 16 t

ORIGIN

Query Match 57.6% Score 14.4; DB 6; Length 24;
 Best local Similarity 75.8%; Pred. No. 9.8e+04;
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0

CY 1 TTTCTTTTATGATGCTG 24
 |||||
 2 TTTCTTTTATGATGCTG 25

Db

RESULT 12
 LOCUS A62421 21 bp DNA linear PAT 04 APR 1999
 DEFINITION Sequence 2 from Patent WO9713974.
 ACCESSION A62421
 VERSION A62421.1 GI:1716353
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 1 (bases 1 to 31)
 REFERENCE
 1 (bases 1 to 31)
 AUTHORS Weindell, K.
 TITLE METHOD OF IDENTIFYING A SUBSTRATE TO BE ANALYZED
 JOURNAL Patent: WO 9713974 A 2 17 APR 1997
 AUTHOR BOEHRINGER MANNHEIM GMBH (DE)
 INVENTOR BOEHRINGER MANNHEIM GMBH (DE)
 APPLICANT BOEHRINGER MANNHEIM GMBH (DE)
 LOCATION/Qualifiers location/Qualifiers

FEATURES
 source 1..31
 /organism="unidentified"
 /db_xref="taxon:32644"

BASE COUNT 3 a 2 c 9 g 17 t

source 1.25

/organelle="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 2 a 7 c 5 g 11 t

ORIGIN

Query Match 59.2%, Score 14.8; Db 6; Length 25;
Best Local Similarity 89.9%; Pred. No. 6.5e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGATGCTG 18
|||||
7 TTTCTTTCATGATGCTG 24

RESULT 4

AX476113

LOCUS AX476113 25 bp DNA linear FAT 12 AUG 2002

DEFINITION Sequence 1337 from Patent WO0224750.

ACCESSION AX476113

VERSION AX476113.1 GI:2215401

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TIME

JOURNAL

FEATURES

source

1.25
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 3 a 6 c 5 g 11 t

ORIGIN

Query Match 59.2%, Score 14.8; Db 6; Length 25;
Best Local Similarity 89.9%; Pred. No. 6.5e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGATGCTG 18
|||||
6 TTTCTTTCATGATGCTG 23

RESULT 5

AX476114

LOCUS AX476114 25 bp DNA linear FAT 12 AUG 2002

DEFINITION Sequence 1337 from Patent WO0224750.

ACCESSION AX476114

VERSION AX476114.1 GI:2215401

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TIME

JOURNAL

FEATURES

source

1.25
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 3 a 6 c 5 g 11 t

ORIGIN

Query Match 59.2%, Score 14.8; Db 6; Length 25;
Best Local Similarity 89.9%; Pred. No. 6.5e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGATGCTG 18
|||||
5 TTTCTTTCATGATGCTG 22

RESULT 6

AX476115

LOCUS AX476115 25 bp DNA linear FAT 12 AUG 2002

DEFINITION Sequence 1337 from Patent WO0224750.

ACCESSION AX476115

VERSION AX476115.1 GI:2215401

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TIME

JOURNAL

FEATURES

source

1.25
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 4 a 6 c 5 g 9 t

ORIGIN

Query Match 59.2%, Score 14.8; Db 6; Length 25;
Best Local Similarity 89.9%; Pred. No. 6.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGATGCTG 18
|||||
4 TTTCTTTCATGATGCTG 21

RESULT 7

AX476116

LOCUS AX476116 25 bp DNA linear FAT 12 AUG 2002

DEFINITION Sequence 1337 from Patent WO0224750.

ACCESSION AX476116

VERSION AX476116.1 GI:2215401

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TIME

JOURNAL

FEATURES

source

1.25
/organism="Homo sapiens"
/db_xref="taxon:9606"

BASE COUNT 5 a 5 c 6 g 9 t

ORIGIN

Query Match 59.2%, Score 14.8; Db 6; Length 25;
Best Local Similarity 89.9%; Pred. No. 6.5e+04;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1 TTTCTTTTATGATGCTG 18
|||||
3 TTTCTTTCATGATGCTG 20

RESULT 8

AX476117

LOCUS AX476117 25 bp DNA linear FAT 12 AUG 2002

966	10.6	42.4	20.6	AP00000
797	10.6	42.4	20.6	AP00001
798	10.6	42.4	20.6	AP00002
800	10.6	42.4	20.6	AP00003
801	10.6	42.4	20.6	AP00004
802	10.6	42.4	20.6	AP00005
803	10.6	42.4	20.6	AP00006
804	10.6	42.4	20.6	AP00007
805	10.6	42.4	20.6	AP00008
806	10.6	42.4	20.6	AP00009
807	10.6	42.4	20.6	AP00010
808	10.6	42.4	20.6	AP00011
809	10.6	42.4	20.6	AP00012
810	10.6	42.4	20.6	AP00013
811	10.6	42.4	20.6	AP00014
812	10.6	42.4	20.6	AP00015
813	10.6	42.4	20.6	AP00016
814	10.6	42.4	20.6	AP00017
815	10.6	42.4	20.6	AP00018
816	10.6	42.4	20.6	AP00019
817	10.6	42.4	20.6	AP00020
818	10.6	42.4	20.6	AP00021
819	10.6	42.4	20.6	AP00022
820	10.6	42.4	20.6	AP00023
821	10.6	42.4	20.6	AP00024
822	10.6	42.4	20.6	AP00025
823	10.6	42.4	20.6	AP00026
824	10.6	42.4	20.6	AP00027
825	10.6	42.4	20.6	AP00028
826	10.6	42.4	20.6	AP00029
827	10.6	42.4	20.6	AP00030
828	10.6	42.4	20.6	AP00031
829	10.6	42.4	20.6	AP00032
830	10.6	42.4	20.6	AP00033
831	10.6	42.4	20.6	AP00034
832	10.6	42.4	20.6	AP00035
833	10.6	42.4	20.6	AP00036
834	10.6	42.4	20.6	AP00037
835	10.6	42.4	20.6	AP00038
836	10.6	42.4	20.6	AP00039
837	10.6	42.4	20.6	AP00040
838	10.6	42.4	20.6	AP00041
839	10.6	42.4	20.6	AP00042
840	10.6	42.4	20.6	AP00043
841	10.6	42.4	20.6	AP00044
842	10.6	42.4	20.6	AP00045
843	10.6	42.4	20.6	AP00046
844	10.6	42.4	20.6	AP00047
845	10.6	42.4	20.6	AP00048
846	10.6	42.4	20.6	AP00049
847	10.6	42.4	20.6	AP00050
848	10.6	42.4	20.6	AP00051
849	10.6	42.4	20.6	AP00052
850	10.6	42.4	20.6	AP00053
851	10.6	42.4	20.6	AP00054
852	10.6	42.4	20.6	AP00055
853	10.6	42.4	20.6	AP00056
854	10.6	42.4	20.6	AP00057
855	10.6	42.4	20.6	AP00058
856	10.6	42.4	20.6	AP00059
857	10.6	42.4	20.6	AP00060
858	10.6	42.4	20.6	AP00061
859	10.6	42.4	20.6	AP00062
860	10.6	42.4	20.6	AP00063
861	10.6	42.4	20.6	AP00064
862	10.6	42.4	20.6	AP00065
863	10.6	42.4	20.6	AP00066
864	10.6	42.4	20.6	AP00067
865	10.6	42.4	20.6	AP00068
866	10.6	42.4	20.6	AP00069
867	10.6	42.4	20.6	AP00070
868	10.6	42.4	20.6	AP00071

[illegible]

869	10.6	42.4	25	6	AX0427765
870	10.6	42.4	25	6	AX0429000
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90	12.6	51.2	25	6	AX476368	Sequence	AX476368	Sequence	C	164	12.2	48.8	34	6	AX476368	Sequence
91	12.6	51.2	25	6	AX476378	Sequence	AX476378	Sequence	C	165	12.2	48.8	34	6	AX476378	Sequence
92	12.6	51.2	25	6	AX476388	Sequence	AX476388	Sequence	C	166	12.2	48.8	34	6	AX476388	Sequence
93	12.6	51.2	25	6	AX476398	Sequence	AX476398	Sequence	C	167	12.2	48.8	34	6	AX476398	Sequence

ORGANISM

REFERENCE

Mus musculus
 Fukuyama, M., Marzari, G., Chardat, G., Gnanata, V., Vertepata, E., Fellecchini,
 Mammalia; Eutheria; Rodentia; Sciurognathia; Muridae; Mus.
 1 (bases 1 to 27)

AUTHORS

TITLE

JOURNAL

COMMENT

Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 208, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunne@genetics.utah.edu
 Insert length: 10000 Std Error: 0.00
 Plate: 0080 Row: 0 Column: 08
 Seq primer: CTTGTAAATCAACGACGAGT
 Class: plasmid ends
 High quality sequence stop: 27.
 Location/Qualifiers

FEATURES

Source

1..27
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="MUG2M090008"
 /clone_lib="Mouse 10kb plasmid mUG2M library"
 /sex="Male"
 /lab_host="F. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: pMD42uv. Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/notes/>). The DNA
 was hydrolytically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapted DNA was purified and size selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD42 (g[472114]g[AF199221]), a copy number
 inducible derivative of plasmid p1. The vector was ligated
 with adaptors complementary to the insert adaptors and
 purified. The sheared, adapted mouse DNA was annealed to
 adaptor vector DNA, and transformed into
 chemically-competent F. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT

12 a 6 c 8 g 1 t

ORIGIN

Query Match

42.48; Score 10.6; E-17; Length 27;

Best local similarity 76.5%; Pred. No. 9.7e+05;

Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY

6 GAGCCGAGAAAGATGAG 22

DB

3 GAGCCGAGAAAGATGAG 19

Search completed: July 21, 2003, 15:48:14
 Job time: 665.467 secs

[illegible][illegible]

0.005 inch efficiency. The sheared DNA was blunt end repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 2.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD19 (31433214) (AF033722), a copy-number inducible derivative of plasmid p1. The vector was ligated with adapters complementary to the insert adapters and purified. The sheared, adapter-mouse DNA was annealed to adapter vector DNA and transformed into chemically-competent *Escherichia coli* (Stratagene) cells and selected for ampicillin resistance.

BASE COUNT

0 a 12 6 3 14 1

Query Match 43.2% Score 10.8; DB 17; Length 32;
Best Local Similarity 85.7% Pred No. 8.3e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 CACAGAAATGAG 23
|||||
28 CACAGAAATGAG 15

RESULT 31

Accession A032495 22 bp mRNA linear EST of A032495
DEFINITION BED0003469 3', mRNA sequence.

ACCESSION A032495 22 bp mRNA linear EST of A032495
DEFINITION BED0003469 3', mRNA sequence.

VERSION A032495.1 22 bp mRNA linear EST of A032495
KEYWORDS EST.
SOURCE house mouse
ORGANISM Mus musculus

REFERENCE Kato, K., Matsuda, T., Hara, T., Taniguchi, T., Endo, T., Mammalia; Eutheria; Rodentia; Scurionanthi; Muridae; Murinae; Mus.
1 (bases 1 to 33)

JOURNAL Kato, K., Matsuda, T., Hara, T., Taniguchi, T., Endo, T., Mammalia; Eutheria; Rodentia; Scurionanthi; Muridae; Murinae; Mus.
1 (bases 1 to 33)

COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5580
Email: kkat@nara.ac.jp,
http://www2.nara.ac.jp/REF/index.html

FEATURES
Location/Qualifiers
1..33
/organism="Mus musculus"

BASE COUNT
16 a 5 c 7 g 5 t

ORIGIN
Query Match 43.2% Score 10.8; DB 17; Length 32;
Best Local Similarity 85.7% Pred No. 8.3e+05;

Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CACAGAAATGAG 24
|||||
28 CACAGAAATGAG 15

RESULT 32
Accession A032495 22 bp mRNA linear EST of A032495
DEFINITION BED0003469 3', mRNA sequence.

DEFINITION A032495.1 22 bp mRNA linear EST of A032495
ACCESSION BED0003469 3', mRNA sequence.

VERSION A032495.1 22 bp mRNA linear EST of A032495
KEYWORDS EST.
SOURCE house mouse

REFERENCE Kato, K., Matsuda, T., Hara, T., Taniguchi, T., Endo, T., Mammalia; Eutheria; Rodentia; Scurionanthi; Muridae; Murinae; Mus.
1 (bases 1 to 33)

JOURNAL Kato, K., Matsuda, T., Hara, T., Taniguchi, T., Endo, T., Mammalia; Eutheria; Rodentia; Scurionanthi; Muridae; Murinae; Mus.
1 (bases 1 to 33)

COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5580
Email: kkat@nara.ac.jp,
http://www2.nara.ac.jp/REF/index.html

FEATURES
Location/Qualifiers
1..33
/organism="Mus musculus"

BASE COUNT
16 a 5 c 7 g 5 t

ORIGIN
Query Match 43.2% Score 10.8; DB 17; Length 32;
Best Local Similarity 85.7% Pred No. 8.3e+05;

Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CACAGAAATGAG 21
|||||
28 CACAGAAATGAG 15

RESULT 33
Accession A032495 24 bp mRNA linear EST of A032495
DEFINITION BED0003469 3', mRNA sequence.

ACCESSION A032495 24 bp mRNA linear EST of A032495
DEFINITION BED0003469 3', mRNA sequence.

VERSION A032495.1 24 bp mRNA linear EST of A032495
KEYWORDS EST.
SOURCE human

REFERENCE Kato, K., Matsuda, T., Hara, T., Taniguchi, T., Endo, T., Mammalia; Eutheria; Rodentia; Scurionanthi; Muridae; Murinae; Mus.
1 (bases 1 to 34)

JOURNAL Kato, K., Matsuda, T., Hara, T., Taniguchi, T., Endo, T., Mammalia; Eutheria; Rodentia; Scurionanthi; Muridae; Murinae; Mus.
1 (bases 1 to 34)

COMMENT Contact: Kikuya Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
8916-5 Takayama, Ikoma, Nara 630-0101, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5580
Email: kkat@nara.ac.jp,
http://www2.nara.ac.jp/REF/index.html

FEATURES
Location/Qualifiers
1..34
/organism="Homo sapiens"

BASE COUNT
16 a 5 c 7 g 5 t

ORIGIN
Query Match 43.2% Score 10.8; DB 17; Length 32;
Best Local Similarity 85.7% Pred No. 8.3e+05;

Matches 15; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 CACAGAAATGAG 24
|||||
28 CACAGAAATGAG 15

RESULT 34
Accession A032495 24 bp mRNA linear EST of A032495
DEFINITION BED0003469 3', mRNA sequence.

[illegible][illegible]

Email: eckert@alk.edu
 This is single pass sequence recovered from the left portion of
 TMA. This sequence lies within 300 bases of the 3' end of
 At4g31770
 Class: TMA tagged
 Location/Qualifiers
 1..30
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"
 /db_xref="taxon:3709"
 /clone="At4g31770.28.95.X"
 /note="1kb Arabidopsis thaliana TMA insertion lines"
 /note="PCR was performed on Arabidopsis thaliana lines
 each of which contains one or more TMA insertion
 elements. The resultant fragment for each line was
 directly sequenced to determine the genomic sequence at
 the site of insertion. Details of the protocols used can
 be found at http://signal.salk.edu/thma_protocols.html"

BASE COUNT

5 a 11 c 4 g 10 t

ORIGIN

Query Match 44.0% Score 11; DB 17; Length 30;
 Best Local Similarity 73.7% Pct. Id. 67.3%
 Matches 11; Conservative 0; Mismatches 5; Gaps 0;
 Db 7 AGCTTCGATGATGAGGAC 12

RESULT 21
 AZ63965/c 33 bp DNA 11 year GSS 14-DEC-2000
 LOCUS 1054391P Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCGM054391P R. DNA sequence.
 ACCESSION AZ63965.1 GI:11801011
 VERSION 1.0
 KEYWORDS house mouse
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 1 (bases 1 to 33)
 REFERENCE
 Dunn, D., Aoyagi, A., Rauber, M., Kuchnir, T., Ewald, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Peilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., St. G.
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: adumag@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate 0643 Row P Column 11
 Seq primer: GACACAGGAAACGCTATGAC
 Class: plasmid ends
 High quality sequence stop: 31.
 Location/Qualifiers
 1..33
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM054391P"
 /clone_1kb="mouse 10kb plasmid UUCGM library"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /note="Vector: pMD22uv; Purified genomic DNA from M."

FEATURES

source

1..31
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM054391P"
 /clone_1kb="mouse 10kb plasmid UUCGM library"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /note="Vector: pMD22uv; Purified genomic DNA from M."

BASE COUNT

10 a 1 c 8 g 12 t

ORIGIN

Query Match 44.0% Score 11; DB 17; Length 31;
 Best Local Similarity 73.7% Pct. Id. 67.4%
 Matches 11; Conservative 0; Mismatches 5; Gaps 0;
 Db 7 AGCTTCGATGATGAGGAC 12

RESULT 21
 AZ63965/c 33 bp DNA 11 year GSS 14-DEC-2000
 LOCUS 1054391P Mouse 10kb plasmid UUCGM library Mus musculus genomic
 DEFINITION clone UUCGM054391P R. DNA sequence.
 ACCESSION AZ63965.1 GI:11801011
 VERSION 1.0
 KEYWORDS house mouse
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 1 (bases 1 to 33)
 REFERENCE
 Dunn, D., Aoyagi, A., Rauber, M., Kuchnir, T., Ewald, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Peilly,
 M., Rose, M., Rose, R., Stokes, R., Tinney, A., von Niederhausern, A.
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., St. G.
 84112, USA
 Tel.: 801 585 5606
 Fax: 801 585 7177
 Email: adumag@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate 0643 Row P Column 11
 Seq primer: GACACAGGAAACGCTATGAC
 Class: plasmid ends
 High quality sequence stop: 33.
 Location/Qualifiers
 1..33
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM054391P"
 /clone_1kb="mouse 10kb plasmid UUCGM library"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /note="Vector: pMD22uv; Purified genomic DNA from M."

FEATURES

source

1..33
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUCGM054391P"
 /clone_1kb="mouse 10kb plasmid UUCGM library"
 /sex="male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /note="Vector: pMD22uv; Purified genomic DNA from M."

musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (<http://www.jax.org/resources/documents/queries/>). The DNA
 was hybridized and screened by repeated passage through a
 0.06 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with 14 DNA polymerase and 14
 polynucleotide kinase. Adaptor oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 ligated DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (414721147b/AP12474.1), a copy-number of
 inducible derivative of plasmid R1. The vector was ligated
 with adaptor complementary to the insert adaptors and
 purified. The sheared, adaptor mouse DNA was annealed to
 adaptor vector DNA and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Email: dunnagenetics.utah.edu
 Insert Length: 1000 bp Error: 0.00
 Plates: 0165 Low: 2 columns 15
 Seq primer: CACACAGCAACACATATGACG
 Class: Plasmid ends
 High quality sequence stop: 27

FEATURES

Location/Qualifiers

1..27

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="MIM155815"

/clone_1ib="mouse 10kb plasmid library"

/sex="Male"

/date="1994-01-01"

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/date="1994-01-01"

/date="1994-01-01"

Email: dunnagenetics.utah.edu
 Insert Length: 1000 bp Error: 0.00
 Plates: 0086 Low: A column 12
 Seq primer: CATTCTAAACGACACGACAT
 Class: Plasmid ends
 High quality sequence stop: 30

FEATURES

Location/Qualifiers

1..30

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="MIM258512"

/clone_1ib="mouse 10kb plasmid library"

/sex="Male"

/date="1994-01-01"

/date="1994-01-01"

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/date="1994-01-01"

Query Match 44.0% Score 11: 10 17: Length 27:
 Best Local Similarity: 73.7% Fied. Hs. 6.6e-05
 Matches 14: Conservative 0: Mismatches 5: Indels 0: Gaps 0:
 4 CAGGACGCAAAAGAGAGAG 22
 4 CAGGACGCAAAAGAGAGAG 22

RESULT 18
 A2817062/1 20 bp DNA linear GEN 20 FEB 2001
 LOCUS A2817062 20 bp DNA linear GEN 20 FEB 2001
 DEFINITION A2817062 1 nt 12000000
 ACCESSION A2817062 1 nt 12000000
 VERSION A2817062 1 nt 12000000
 KEYWORDS mouse muscle
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa;
 Mammalia; Furberia; Rodentia; Sciurognathi; Murina; Muridae;
 1 (bases 1 to 20)
 Danu, D., Ayay, A., Parker, M., Pearson, T., Dival, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Muehlen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, P., Stokes, F., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 Mouse whole genome draft: 1000 with failed and reads from 1000
 Plasmid inserts
 Unpublished (2000)
 CONTACT Robert E. Weiss
 University of Utah Genome Center
 University of Utah
 Pm. 104, Rm. 1111
 Salt Lake City, UT 84142, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

Query Match 44.0% Score 11: 10 17: Length 27:
 Best Local Similarity: 73.7% Fied. Hs. 6.6e-05
 Matches 14: Conservative 0: Mismatches 5: Indels 0: Gaps 0:
 4 CAGGACGCAAAAGAGAG 22
 4 CAGGACGCAAAAGAGAG 22

RESULT 19
 B0709054/1 20 bp DNA linear GEN 20 FEB 2001
 LOCUS B0709054 20 bp DNA linear GEN 20 FEB 2001
 DEFINITION B0709054 1 nt 12000000
 ACCESSION B0709054 1 nt 12000000
 VERSION B0709054 1 nt 12000000
 KEYWORDS mouse muscle
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Eumetazoa;
 Mammalia; Furberia; Rodentia; Sciurognathi; Murina; Muridae;
 1 (bases 1 to 20)
 Danu, D., Ayay, A., Parker, M., Pearson, T., Dival, B., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Muehlen, E., Pedersen, T., Reilly,
 M., Rose, M., Rose, P., Stokes, F., Tingey, A., von Niederhausen, A.
 and Wright, D., Weiss, R.
 Mouse whole genome draft: 1000 with failed and reads from 1000
 Plasmid inserts
 Unpublished (2000)
 CONTACT Robert E. Weiss
 University of Utah Genome Center
 University of Utah
 Pm. 104, Rm. 1111
 Salt Lake City, UT 84142, USA
 Tel: 801 585 5606
 Fax: 801 585 7177

/db_xref="taxon:10090"
 /clone="Mmu2M008100s"
 /clone_lib="Mouse 10kb plasmid library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /vector="pCMVcat. Purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD18 (41473214) (pMD18.1) (a 2.9 kb) by the inducible derivative of plasmid p1. The vector was ligated with adapter complementary to the insert adapters and purified. The sheared, adapter-mouse DNA was annealed to chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 12 A 6 C 13 G 6 T

ORIGIN

Query Match 46.4% Score 11.6 E-17 Length 31
 Best Local Similarity 77.8% Pred. No. 4.1e+05
 Matches 14 Conservative 0 Mismatches 4 Indels 0 Gaps 0

CY 2 ACCGACAAATGACT 24
 1 |||||
 2 ACGACAAATGACT 19

Db

RESULT 9
 TATACG1P/c
 LOCUS
 DEFINITION
 TATACG1P 24 bp DNA linear GSS 13 DEC 2000
 T. Brucei sheared genomic DNA clone (mouse), forward sequence,
 genomic survey sequence.
 ACCESSION
 M461940
 VERSION
 AL461940.1 GI11860981
 KEYWORDS
 GSS
 SOURCE
 Trypanosoma brucei
 ORGANISM
 Trypanosoma brucei
 Puberty, T. brucei, Kinetoplast, Trypanosomatidae,
 Trypanosoma,
 1 (bases 1 to 24)
 Hall, N., Rowan, S., Leonard, N., DePamphilis, A., Atkin, P.,
 Chillingworth, C., Ormond, D., Harris, R., El-Sayed, N., Hou, L.,
 Melville, S.E., Pandey, M.A. and Batteelli, B.G.
 Direct Submission
 Submitted (11 Dec 2000) Trifluoroacetic acid gel electrophoresis
 Project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
 Cambridge CB10 1SA. E-mail: batteelli@sanger.ac.uk and
 nhls@sanger.ac.uk
 Constructed at the Institute for Genome Research (HGP),
 Rockville, MD. Genomic DNA isolated from a cloned population of
 Trypanosoma brucei (TATACG1P/c) is 11 was mechanically sheared
 to give a light size distribution (4 kb). The V.1 method used for the library construction is
 described in detail in Smith, H. and Venter, O.C. (Making small
 insert libraries for whole genome shotgun sequencing projects. In
 Genome Sequencing: A Practical Approach, eds M. Vardan and R.
 Batteelli, Oxford University Press, 1999).
 Email: nhls@sanger.ac.uk
 Details of T. brucei sequencing at the Sanger Centre are available
 at <http://www.sanger.ac.uk/Genome/Trifluoroacetic%20acid>
 Location/Qualifiers

FEATURES
 1..24
 /organism="Trypanosoma brucei"
 /strain="TBE0927"

/db_xref="taxon:5691"
 /clone="7B003"
 /clone_lib="Mus 10kb plasmid library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /vector="pCMVcat. Purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD18 (41473214) (pMD18.1) (a 2.9 kb) by the inducible derivative of plasmid p1. The vector was ligated with adapter complementary to the insert adapters and purified. The sheared, adapter-mouse DNA was annealed to chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 11 A 6 C 12 G 2 T

ORIGIN

Query Match 46.4% Score 11.6 E-17 Length 31
 Best Local Similarity 77.8% Pred. No. 4.1e+05
 Matches 14 Conservative 0 Mismatches 4 Indels 0 Gaps 0

CY 2 ACCGACAAATGACT 24
 1 |||||
 2 ACGACAAATGACT 19

Db

RESULT 10
 AA920864
 LOCUS
 DEFINITION
 AA920864 31 bp mRNA linear EST 20 APR 1999
 Mus musculus, clone IMAGE1332876, similar to Tr-01003 (GenBank) mRNA.
 ACCESSION
 AA920864
 VERSION
 AA920864.1 GI11860981
 KEYWORDS
 EST
 SOURCE
 house mouse,
 Mus musculus
 ORGANISM
 Mus musculus
 Buiatova, Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
 Mammalia; Eutheria; Rodentia; Sciurophathi; Muridae; Murinae; Mus.
 1 (bases 1 to 31)
 Maita, M., Hillier, L., Allen, M., Bowles, M., Donnelly, N., Fehrmann,
 Gaisell, S., Foychuk, T., Levy, M., Li, M., Maitland, M., Maitland,
 Schellenger, K., Stepien, M., Tan, F., Underwood, R., Moore, R.,
 Tholisinger, R., White, T., Leach, G., Soares, J., Wilson, R. and
 Waterston, R.
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Maria M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 444 Forest Park Parkway, Box 8001, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through INM; contact the
 IMAGE Consortium (info@image.llnwd.net) for further information.
 MGI:683172
 Trace (Sanger) (overall) poor quality
 Possible reversed (left) strand
 Seq primer: 26m13 rev1 ET from Amsterdam
 High quality sequence stop: 1.
 Location/Qualifiers

FEATURES
 1..31
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="7B003"
 /clone_lib="Mus 10kb plasmid library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
 /vector="pCMVcat. Purified genomic DNA from Mus musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrolytically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD18 (41473214) (pMD18.1) (a 2.9 kb) by the inducible derivative of plasmid p1. The vector was ligated with adapter complementary to the insert adapters and purified. The sheared, adapter-mouse DNA was annealed to chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
 11 A 6 C 12 G 2 T

ORIGIN

Query Match 46.4% Score 11.6 E-17 Length 31
 Best Local Similarity 77.8% Pred. No. 4.1e+05
 Matches 14 Conservative 0 Mismatches 4 Indels 0 Gaps 0

CY 4 CCGACAAATGACT 24
 1 |||||
 2 ACGACAAATGACT 19

Db

RESULT 26
 CCGACAAATGACT 24
 1 |||||
 2 ACGACAAATGACT 19

Db

RESULT 26
 CCGACAAATGACT 24
 1 |||||
 2 ACGACAAATGACT 19

City Water 47.09 6.14 12.8 5P.10 100%
East Local Similarity 66.64 Not 100%
Metals 16, Carbon 100 % Nitrogen 100 %

Cy 3 TTTTGGGCTTAAAGATTATGTC TC
Dh 11111111111111111111
29 TCGAAGCCTTAAGATTGTGC G

[illegible][illegible]

[illegible]

Journal of Management Inquiry 26(10) 1000-1017 © The Author(s) 2017. Reprints and permissions: sagepub.com/journalsPermissions.nav DOI: 10.1177/1056492617730001

[illegible]

[illegible]

80	10.2	40.6	34.0	AV947172	AV947172	152	9.6	39.4	29.1	EH949474
81	10.2	40.6	34.0	AV947172	AV947172	153	9.6	39.4	29.1	EH949474
82	10.2	40.6	34.0	AV947172	AV947172	154	9.6	39.4	29.1	EH949474
83	10.2	40.6	34.0	AV947172	AV947172	155	9.6	39.4	29.1	EH949474
84	10.2	40.6	34.0	AV947172	AV947172	156	9.6	39.4	29.1	EH949474
85	10.2	40.6	34.0	AV947172	AV947172	157	9.6	39.4	29.1	EH949474
86	10.2	40.6	34.0	AV947172	AV947172	158	9.6	39.4	29.1	EH949474
87	10.2	40.6	34.0	AV947172	AV947172	159	9.6	39.4	29.1	EH949474
88	10.2	40.6	34.0	AV947172	AV947172	160	9.6	39.4	29.1	EH949474
89	10.2	40.6	34.0	AV947172	AV947172	161	9.6	39.4	29.1	EH949474
90	10.2	40.6	34.0	AV947172	AV947172	162	9.6	39.4	29.1	EH949474
91	10.2	40.6	34.0	AV947172	AV947172	163	9.6	39.4	29.1	EH949474
92	10.2	40.6	34.0	AV947172	AV947172	164	9.6	39.4	29.1	EH949474
93	10.2	40.6	34.0	AV947172	AV947172	165	9.6	39.4	29.1	EH949474
94	10.2	40.6	34.0	AV947172	AV947172	166	9.6	39.4	29.1	EH949474
95	10.2	40.6	34.0	AV947172	AV947172	167	9.6	39.4	29.1	EH949474
96	10.2	40.6	34.0	AV947172	AV947172	168	9.6	39.4	29.1	EH949474
97	10.2	40.6	34.0	AV947172	AV947172	169	9.6	39.4	29.1	EH949474
98	10.2	40.6	34.0	AV947172	AV947172	170	9.6	39.4	29.1	EH949474
99	10.2	40.6	34.0	AV947172	AV947172	171	9.6	39.4	29.1	EH949474
100	10.2	40.6	34.0	AV947172	AV947172	172	9.6	39.4	29.1	EH949474
101	10.2	40.6	34.0	AV947172	AV947172	173	9.6	39.4	29.1	EH949474
102	10.2	40.6	34.0	AV947172	AV947172	174	9.6	39.4	29.1	EH949474
103	10.2	40.6	34.0	AV947172	AV947172	175	9.6	39.4	29.1	EH949474
104	10.2	40.6	34.0	AV947172	AV947172	176	9.6	39.4	29.1	EH949474
105	10.2	40.6	34.0	AV947172	AV947172	177	9.6	39.4	29.1	EH949474
106	10.2	40.6	34.0	AV947172	AV947172	178	9.6	39.4	29.1	EH949474
107	10.2	40.6	34.0	AV947172	AV947172	179	9.6	39.4	29.1	EH949474
108	10.2	40.6	34.0	AV947172	AV947172	180	9.6	39.4	29.1	EH949474
109	10.2	40.6	34.0	AV947172	AV947172	181	9.6	39.4	29.1	EH949474
110	10.2	40.6	34.0	AV947172	AV947172	182	9.6	39.4	29.1	EH949474
111	10.2	40.6	34.0	AV947172	AV947172	183	9.6	39.4	29.1	EH949474
112	10.2	40.6	34.0	AV947172	AV947172	184	9.6	39.4	29.1	EH949474
113	10.2	40.6	34.0	AV947172	AV947172	185	9.6	39.4	29.1	EH949474
114	10.2	40.6	34.0	AV947172	AV947172	186	9.6	39.4	29.1	EH949474
115	10.2	40.6	34.0	AV947172	AV947172	187	9.6	39.4	29.1	EH949474
116	10.2	40.6	34.0	AV947172	AV947172	188	9.6	39.4	29.1	EH949474
117	10.2	40.6	34.0	AV						

2b 24 CCGTGGAGCCGAGAAAGATGAGT 1

RESULT 38
US-09-771-933 8

Sequence 8, Application US/02/0015112
Publication No. US2003009296A1
GENERAL INFORMATION:
APPLICANT: Gill-Garrison, Rosalynn F
APPLICANT: Martin, Christopher J
APPLICANT: Sanchez Felix, Manuel V
TITLE OF INVENTION: Computer assisted means for assessing lifestyle risk
FILE REFERENCE: 620-110
CURRENT APPLICATION NUMBER: US/02/771/933
CURRENT FILING DATE: 11/01/02
NUMBER OF SEQ ID NOS: 205
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO: 8
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-771-933 8

Query Match 51.2%, Score 12.8, DB 15, Length 25,
Best Local Similarity 78.8%, Pred. No. 1.2e+04,
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

QY 1 CCGTGGAGCCGAGAAAGATGAGT 24
2 CCGTGGAGCCGAGAGTGGAGT 25

RESULT 39

US-10-081-119-11/c
Sequence 11, Application US/10081119
Publication No. US2003004591A1
GENERAL INFORMATION:
APPLICANT: Reinhard, Christoph
APPLICANT: Jefferson, Anne B.
APPLICANT: Chan, Vivien W.
TITLE OF INVENTION: TTK in diagnosis and as a therapeutic
FILE REFERENCE: 16932.002
CURRENT APPLICATION NUMBER: US/10/081-119
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 60/289,813
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 11
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthesized oligonucleotide
US-10-081-119-11

Query Match 51.2%, Score 12.8, DB 15, Length 25,
Best Local Similarity 87.5%, Pred. No. 1.2e+04,
Matches 14, Conservative 0, Mismatches 2, Indels 0, Gaps 0;

QY 7 AGCCCTGAAGATGAG 22
17 AGCCCTGAAGATGAG 2

RESULT 40
US-10-215-112-5162/c

Sequence 5162, Application US/02/0015112
Publication No. US2003009296A1
GENERAL INFORMATION:
APPLICANT: Michael Miltmann
TITLE OF INVENTION: Method of Genetic Analysis of Proteins
FILE REFERENCE: 3119
CURRENT APPLICATION NUMBER: US/02/0015112
CURRENT FILING DATE: 06/08/08
NUMBER OF SEQ ID NOS: 14916
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 5162
LENGTH: 25
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized oligonucleotide
US-10-215-112-5162

Query Match 51.2%, Score 12.8, DB 15, Length 25,
Best Local Similarity 78.8%, Pred. No. 1.2e+04,
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

QY 1 CCGTGGAGCCGAGAAAGATGAGT 24
24 CCGTGGAGCCGAGAGTGGAGT 1

Search completed: July 23, 2003, 18:39:35
CPU time: 68.3940 secs

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1 ORGANISM: Artificial Sequence
2 FEATURE:
3 OTHER INFORMATION: Description of Artificial Sequence:
4 OTHER INFORMATION: for information of a nucleotide data base
US-09-925-988-32

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Query Match          52.0%, Score 13, DB 12, Length 30
Best Local Similarity 76.2%, Ident. No. 9,440+03,
Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

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CY 1 GGTCCGAGCCGAGAGATGATCA 21
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DB 6 CATGAGAGCCGAGAGAGATGATCA 26

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RESULT 34

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US-10-138-634-11
1 Sequence 13, Application US/02038903
2 Patent No. US2001004936A1
3 GENERAL INFORMATION:
4 APPLICANT: KOBAYASHI, Toshinide
5 APPLICANT: KIYOSAWA, Shiro
6 APPLICANT: HASEGAWA, Akiro
7 TITLE OF INVENTION: Anti-viral Defensing Film
8 FILE REFERENCE: P2304
9 CURRENT AFFILIATION NUMBER: 2001-000004
10 CURRENT FILING DATE: 2001-01-18
11 PRIORITY AFFILIATION NUMBER: 2001-000004
12 PRIORITY FILING DATE: 2001-01-18
13 PRICE AFFILIATION NUMBER: 2001-000004
14 PRICE FILING DATE: 2001-01-18
15 NUMBER OF SEQ ID NOS: 12
16 SOFTWARE: Patent In Version 3.0
17 SEQ ID NO 11
18 LENGTH: 30
19 TYPE: DNA
20 ORGANISM: Artificial Sequence
21 FEATURE:
22 OTHER INFORMATION: Primer
23 NAME/KEY: n
24 LOCATION: (10...130)
25 OTHER INFORMATION: n is any base
US-10-138-634-11

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Query Match          52.0%, Score 13, DB 12, Length 30
Best Local Similarity 76.2%, Ident. No. 9,440+03,
Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

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CY 2 TCGAGAGCCGAGAGATGATGACT 24
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DB 2 TCGAGAGCCGAGAGATGATGACT 23

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RESULT 35

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US-09-949-076-97-2
1 Sequence 87, Application US/00049016
2 Patent No. US2001004936A1
3 GENERAL INFORMATION:
4 APPLICANT: Sebhel, Peter
5 APPLICANT: Dammann, Nicolas
6 APPLICANT: Bachmann, Martin
7 APPLICANT: Tissot, Alain
8 APPLICANT: Lechner, Franziska
9 TITLE OF INVENTION: Metastatic Antigen Array
10 FILE REFERENCE: 1700-0188002
11 CURRENT AFFILIATION NUMBER: 2001-000004
12 CURRENT FILING DATE: 2001-05-05
13 NUMBER OF SEQ ID NOS: 146
14 SOFTWARE: Patent In Ver. 2.1
15 SEQ ID NO 87
16 LENGTH: 33
17 TYPE: DNA

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1 ORGANISM: Artificial Sequence
2 FEATURE:
3 OTHER INFORMATION: Primer
US-09-848-616-87

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Query Match          52.0%, Score 13, DB 12, Length 30
Best Local Similarity 76.2%, Ident. No. 9,440+03,
Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

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CY 5 CGAGCCGAGAGAGATGAGTGC 25
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DB 29 CTAGGAGAGAGAGATGAGTGC 9

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RESULT 36

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US-09-426-548-13/C
1 Sequence 13, Application US/09426548
2 Patent No. US2001004936A1
3 GENERAL INFORMATION:
4 APPLICANT: Robbins, David
5 APPLICANT: Lin-Geerke, Jull L.
6 APPLICANT: Ling, Jessica
7 TITLE OF INVENTION: NO: US2001004936A1 Mutations in Human MDM and MDM2 genes used
8 FILE REFERENCE: DEX 0054
9 CURRENT AFFILIATION NUMBER: 2001-000004
10 CURRENT FILING DATE: 1999-10-02
11 NUMBER OF SEQ ID NOS: 132
12 SOFTWARE: Patent In Ver. 2.0
13 SEQ ID NO 13
14 LENGTH: 24
15 TYPE: DNA
16 ORGANISM: Homo sapiens
US-09-426-548-13

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Query Match          52.0%, Score 13, DB 12, Length 30
Best Local Similarity 76.2%, Ident. No. 9,440+03,
Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

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CY 2 GTCCGAGCCGAGAGATGATG 22
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DB 32 GTTAAATGAGAGAGATGATG 12

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RESULT 37

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US-09-172-442-07/C
1 Sequence 17, Application US/000711933
2 Patent No. US2001004936A1
3 GENERAL INFORMATION:
4 APPLICANT: Gill, Garthson, Rodalynn D
5 APPLICANT: Martin, Christopher J
6 APPLICANT: Sanchez Felix, Manuel V
7 TITLE OF INVENTION: Cytokeratin-associated Means for Assessing Tumor Size
8 FILE REFERENCE: 620-130
9 CURRENT AFFILIATION NUMBER: 2001-000004
10 CURRENT FILING DATE: 2001-01-30
11 NUMBER OF SEQ ID NOS: 205
12 SOFTWARE: Patent In Ver. 2.1
13 SEQ ID NO 7
14 LENGTH: 25
15 TYPE: DNA
16 ORGANISM: Artificial Sequence
17 FEATURE:
18 OTHER INFORMATION: Description of Artificial Sequence:
19 OTHER INFORMATION: Oligonucleotide
US-09-172-442-07

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```

Query Match          51.2%, Score 12.9, DB 12, Length 25;
Best Local Similarity 70.8%, Ident. No. 1,240+04,
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0,

```

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CY 1 GGTCCGAGCCGAGAGATGATG 24

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RESULT 30
 US-10-198-677-111/6
 Sequence 111: Application US/10-198-677-111/6
 Publication No. US-2001-019-111/6
 GENERAL INFORMATION:
 APPLICANT: CHOI, Yoon
 APPLICANT: KIM, Aaron
 APPLICANT: MOORE, Michael
 TITLE OF INVENTION: METHOD AND SYSTEMS FOR IDENTIFYING AND CHARACTERIZING BY
 TITLE OF INVENTION: SELECTABLE LINKS CONNECTED NUCLEIC ACID SEQUENCES
 TITLE OF INVENTION: SEQUENCES
 FILE REFERENCE: 10/06-2011 / 01-1001
 CURRENT FILING DATE: 2002-07-17
 NUMBER OF SEQ ID NOS: 144
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 111
 LENGTH: 35
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: BCGH23
 US-10-198-677-111

Query Match: 69.89, Score 13.2, DB 15, Length 35
 Best Local Similarity: 88.19, Freq. No. 1, Mismatches: 3, Indels: 0, Gaps: 0
 Matches: 10, Conservative: 0, Mismatches: 3, Indels: 0, Gaps: 0
 QY 6 GAGCCGCAAGAGATGAGT 23
 DB 18 GATCTTAAAAAGATGCGT 1

RESULT 31
 US-06-263B-7806/C
 Sequence 7806: Application US/06-263B-7806/C
 Patent No. US-2000-044-0001
 GENERAL INFORMATION:
 APPLICANT: CHOI, Yoon
 APPLICANT: KIM, Aaron
 APPLICANT: MOORE, Michael
 TITLE OF INVENTION: METHOD AND SYSTEMS FOR IDENTIFYING AND CHARACTERIZING BY
 TITLE OF INVENTION: SELECTABLE LINKS CONNECTED NUCLEIC ACID SEQUENCES
 TITLE OF INVENTION: SEQUENCES
 FILE REFERENCE: 10/06-2011 / 01-1001
 CURRENT FILING DATE: 2002-07-17
 NUMBER OF SEQ ID NOS: 144
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 111
 LENGTH: 35
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: BCGH23
 US-10-198-677-111

RESULT 32
 US-10-198-677-111/6
 Sequence 111: Application US/10-198-677-111/6
 Publication No. US-2001-019-111/6
 GENERAL INFORMATION:
 APPLICANT: CHOI, Yoon
 APPLICANT: KIM, Aaron
 APPLICANT: MOORE, Michael
 TITLE OF INVENTION: METHOD AND SYSTEMS FOR IDENTIFYING AND CHARACTERIZING BY
 TITLE OF INVENTION: SELECTABLE LINKS CONNECTED NUCLEIC ACID SEQUENCES
 TITLE OF INVENTION: SEQUENCES
 FILE REFERENCE: 10/06-2011 / 01-1001
 CURRENT FILING DATE: 2002-07-17
 NUMBER OF SEQ ID NOS: 144
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 111
 LENGTH: 35
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: BCGH23
 US-10-198-677-111

Query Match: 69.89, Score 13.2, DB 15, Length 35
 Best Local Similarity: 88.19, Freq. No. 1, Mismatches: 3, Indels: 0, Gaps: 0
 Matches: 10, Conservative: 0, Mismatches: 3, Indels: 0, Gaps: 0
 QY 4 CGAGCCGCAAGAGATGAGT 24
 DB 1 CGATCTTAAAAAGATGCGT 21

RESULT 33
 US-06-263B-7806/C
 Sequence 7806: Application US/06-263B-7806/C
 Patent No. US-2000-044-0001
 GENERAL INFORMATION:
 APPLICANT: CHOI, Yoon
 APPLICANT: KIM, Aaron
 APPLICANT: MOORE, Michael
 TITLE OF INVENTION: METHOD AND SYSTEMS FOR IDENTIFYING AND CHARACTERIZING BY
 TITLE OF INVENTION: SELECTABLE LINKS CONNECTED NUCLEIC ACID SEQUENCES
 TITLE OF INVENTION: SEQUENCES
 FILE REFERENCE: 10/06-2011 / 01-1001
 CURRENT FILING DATE: 2002-07-17
 NUMBER OF SEQ ID NOS: 144
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 111
 LENGTH: 35
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: BCGH23
 US-10-198-677-111

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1 APPLICATION NUMBER: US-09-982,980A
2 FILING DATE: 14-SEP-2001
3 CLASSIFICATION: <Unknown>
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5 PRIORITY APPLICATION DATA:
6 APPLICATION NUMBER: 09-050,519
7 FILING DATE: <Unknown>
8 APPLICATION NUMBER: US 08/944,445
9 FILING DATE: 18-APR-1997
10 APPLICATION NUMBER: US 08/944,447
11 FILING DATE: 25-APR-1997
12 APPLICATION NUMBER: US 08/944,448
13 FILING DATE: 06-MAY-1997
14 APPLICATION NUMBER: US 08/944,449
15 FILING DATE: 09-MAY-1997
16 APPLICATION NUMBER: US 08/911,312
17 FILING DATE: 14-AUG-1997
18 APPLICATION NUMBER: US 08/911,361
19 FILING DATE: 14-AUG-1997
20 APPLICATION NUMBER: US 08/919,600
21 FILING DATE: 14-AUG-1997
22 APPLICATION NUMBER: US 08/919,643
23 FILING DATE: 19-NOV-1997
24 APPLICATION NUMBER: US 08/974,884
25 FILING DATE: 19-NOV-1997
26 APPLICATION NUMBER: US 08/974,884
27 FILING DATE: 01-OCT-1997
28 FILING DATE: 01-OCT-1997
29
30 ATTORNEY/AGENT INFORMATION:
31 NAME: Parent, Annette S.
32 REGISTRATION NUMBER: 13,859
33 FIRM: PARENT, ANNETTE S. & ASSOCIATES, P.C.
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (415) 576-0300
36 TELEFAX: (415) 576-0300
37
38 INFORMATION FOR SEQ ID NO: 40:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 33 base pairs
41 TYPE: nucleic acid
42 STRANDEDNESS: single
43 TOPOLOGY: linear
44
45 MOLECULE TYPE: other nucleic acid
46 DESCRIPTION: 13a Phosphorothioate oligonucleotide
47
48 SEQUENCE DESCRIPTION: SEQ ID NO: 40:
49 US-09-982,980A
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1 TYPE: DNA
2 ORGANISM: Artificial Sequence
3 FEATURES:
4 OTHER INFORMATION: Description of Artificial Sequence: Protein
5 US-99-052-990A-1
6 Query Match: 52.9% Score 13.27 E9.10 Length 24
7 Best Local Similarity: 63.1% Fred. No: 7.5e+03
8 Matches: 10, Conservative: 0, Mismatches: 4, Indels: 1, gaps: 1
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1 CURRENT FILING DATE: 2001-01-09
2 PRIORITY APPLICATION NUMBER: 2000-05-26
3 PRIORITY FILING DATE: 2000-05-26
4 NUMBER OF SEQ ID NOS: 14694
5 SOFTWARE: MEGA 1.0.6
6 SEQ ID NO: 14694
7 LENGTH: 25
8 TYPE: DNA
9 ORGANISM: Homo sapiens
10 US: 10-098-2638-8574
11
12 Query Match: 55.28% Score: 11.94, 18.25, Length: 30
13 Best Local Similarity: 88.24% Pval: 0.000000
14 Matches: 189 Overlap: 100% Mismatches: 0, Gaps: 0
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[illegible]

US 09-866-108-11980

Query Match: 56.0% Score 14; DB 10; Length 25;
 Best Local Similarity: 77.3% Freq. No. 3,1e+03;
 Matches: 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TCCGAGCCGCAAGAAATGAGGT 24
 |||||
 1 TCCGAGTTATATGAGGAGAGT 22

RESULT 10

US 10-015-112-13122/C
 ; Sequence 13122, Application US/10010112
 ; Publication No. US00033333A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Michael Miltman
 ; TITLE OF INVENTION: Method of Gene Analysis of B-lym-
 ; TITLE OF INVENTION: TERT3
 ; FILE REFERENCE: 3119
 ; CURRENT APPLICATION NUMBER: US/10/215,112
 ; CURRENT FILING DATE: 2002-08-08
 ; NUMBER OF SEQ. ID NOS: 14936
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ. ID NO: 13122
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthesized by the
 US 10-015-112-13122

Query Match: 56.0% Score 14; DB 15; Length 25;
 Best Local Similarity: 77.3% Freq. No. 3,1e+03;
 Matches: 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCCAGCTTAAAGATGAGGT 24
 |||||
 23 GTGAGTATCAAGAAATGAGGT 2

RESULT 11
 US 10-008-203B-45347/C
 ; Sequence 45347, Application US/1000000001
 ; Publication No. US0000000001A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/0000000001
 ; CURRENT FILING DATE: 2003-01-08
 ; PRIOR APPLICATION NUMBER: 60/246,759
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ. ID NOS: 11000
 ; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 ; SEQ. ID NO: 45347
 ; LENGTH: 25
 ; TYPE: DNA
 ; ORGANISM: Homo sapien
 US-10-008-203B-45349

Query Match: 56.0% Score 14; DB 15; Length 25;
 Best Local Similarity: 77.3% Freq. No. 3,1e+03;
 Matches: 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TCCGAGCCGCAAGAAATGAGGT 24
 |||||
 24 TCCGAGTTATATGAGGAGAGT 3

RESULT 12
 US 10-008-263B-45356/C
 ; Sequence 45356, Application US/1000000001

Publication No. US20030104410A1

GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/0000000001
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/246,759
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ. ID NOS: 13106
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ. ID NO: 45356
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US 10-008-263B-45359

Query Match: 56.0% Score 14; DB 15; Length 25;
 Best Local Similarity: 77.3% Freq. No. 3,1e+03;
 Matches: 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TCCGAGCCGCAAGAAATGAGGT 24
 |||||
 24 TCCGAGTTATATGAGGAGAGT 3

Query Match: 56.0% Score 14; DB 15; Length 25;
 Best Local Similarity: 77.3% Freq. No. 3,1e+03;
 Matches: 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 GTCCAGCTTAAAGATGAGGT 24
 |||||
 24 GTGAGTATCAAGAAATGAGGT 3

RESULT 13

US 09-755-830-19
 ; Sequence 19, Application US/09755830
 ; Publication No. US0000000001A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Georgopoulos, Kalia
 ; TITLE OF INVENTION: LAMARCA: A System for High-Throughput
 ; TITLE OF INVENTION: THEROF
 ; FILE REFERENCE: 1998/067001
 ; CURRENT APPLICATION NUMBER: US/09/755,830
 ; CURRENT FILING DATE: 2001-01-05
 ; PRIOR APPLICATION NUMBER: US 09/283,300
 ; PRIOR FILING DATE: 1999-07-26
 ; PRIOR APPLICATION NUMBER: US 08/238,212
 ; PRIOR FILING DATE: 1994-05-02
 ; PRIOR APPLICATION NUMBER: US 06/121,438
 ; PRIOR FILING DATE: 1993-09-14
 ; PRIOR APPLICATION NUMBER: US 07/346,233
 ; PRIOR FILING DATE: 1992-09-14
 ; NUMBER OF SEQ. ID NOS: 43
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ. ID NO: 19
 ; LENGTH: 24
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthesized by the
 US 09-755-830-19

Query Match: 56.2% Score 13.8; DB 11; Length 24;
 Best Local Similarity: 99.2% Freq. No. 3,1e+03;
 Matches: 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GCTCGAGCTTAAAGATGAGGT 17
 |||||
 5 GCTCGAGCTTAAAGATGAGGT 21

RESULT 14

US 10-008-263B-45357/C
 ; Sequence 45357, Application US/1000000001
 ; Publication No. US0000000001A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Miltman, Michael
 ; TITLE OF INVENTION: Human Microarray
 ; FILE REFERENCE: 3118.1
 ; CURRENT APPLICATION NUMBER: US/10/0000000001

PRIOR FILING DATE: 2001-01-30
PRIORITY CLAIMED TO:
PRIORITY DOCUMENT NO.:
PRIORITY FILING DATE: 2001-01-30

966 10.4 41.6 21 10 US-09-765-081-437 Sequence 437, App
 C 967 10.4 41.6 21 10 US-09-810-994-130 Sequence 39, Appl
 968 10.4 41.6 21 10 US-09-844-374-155 Sequence 155, Ap
 C 969 10.4 41.6 21 12 US-09-844-474-445 Sequence 445, Ap
 C 970 10.4 41.6 21 15 US-10-000-014-9 Sequence 9, Appl
 C 971 10.4 41.6 21 15 US-10-135-152-9 Sequence 9, Appl
 C 972 10.4 41.6 21 16 US-10-104-755-46 Sequence 46, Appl
 C 973 10.4 41.6 21 16 US-10-143-516-3 Sequence 3, Appl
 C 974 10.4 41.6 21 15 US-10-068-958-454 Sequence 153, App
 C 975 10.4 41.6 21 15 US-10-070-966-105 Sequence 105, Ap
 C 976 10.4 41.6 22 12 US-09-707-848-9 Sequence 9, Appl
 C 977 10.4 41.6 23 10 US-09-903-156-12 Sequence 12, Appl
 C 978 10.4 41.6 23 10 US-09-987-190-10 Sequence 10, Appl
 C 979 10.4 41.6 23 10 US-09-817-607-66 Sequence 66, Appl
 C 980 10.4 41.6 23 15 US-10-273-707-46 Sequence 46, Appl
 C 981 10.4 41.6 23 15 US-10-109-670-31 Sequence 31, Appl
 C 982 10.4 41.6 24 16 US-09-949-966-143 Sequence 143, App
 C 983 10.4 41.6 24 16 US-09-949-966-143 Sequence 143, App
 C 984 10.4 41.6 24 16 US-09-949-966-143 Sequence 143, App
 C 985 10.4 41.6 24 10 US-09-989-722-143 Sequence 143, App
 986 10.4 41.6 24 10 US-09-989-722-143 Sequence 143, App
 987 10.4 41.6 24 10 US-09-989-722-143 Sequence 143, App
 988 10.4 41.6 24 10 US-09-989-722-143 Sequence 143, App
 989 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 990 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 991 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 992 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 993 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 994 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 995 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 996 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 997 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 998 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 999 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App
 1000 10.4 41.6 24 11 US-09-989-731-143 Sequence 143, App

ALIGNMENTS

RESULT 1
 US-10-098-263B 89794
 ? Sequence 89794, Application US/10098263B
 ? Publication No. US2003010410A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Miltman, Michael
 ? TITLE OF INVENTION: Human Microarray
 ? FILE REFERENCE: 3118-1
 ? CURRENT APPLICATION NUMBER: US/10/098,263B
 ? CURRENT FILING DATE: 2001-01-30
 ? PRIOR APPLICATION NUMBER: 62/776,759
 ? PRIOR FILING DATE: 2001-01-16
 ? NUMBER OF SEQ ID NOS: 11006
 ? SOFTWARE: Vectorway Fit 2.0, Seqman, ClustalX, Gaps 1.1
 ? SEQ ID NO 89794
 ? LENGTH: 25
 ? TYPE: DNA
 ? ORGANISM: Homo sapien
 ? US-10-098-263B 89794
 Query Match 60.8%, Score 15.2, EB 15, Length 25
 Best Local Similarity 60.8%, Seed No. 4, E=0.002
 Matches 17, Conservative 3, Mismatches 3, Indels 0, Gaps 0
 CY 1 CTTGAGGCGCAAGATG 20
 DB |||||||||
 24 CTTGAGGCGCAAGATG 20
 RESULT 2
 US-10-098-263B 89794
 ? Sequence 89794, Application US/10098263B
 ? Publication No. US2003010410A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Miltman, Michael
 ? TITLE OF INVENTION: Human Microarray
 ? FILE REFERENCE: 3118-1
 ? CURRENT APPLICATION NUMBER: US/10/098,263B
 ? CURRENT FILING DATE: 2001-01-30
 ? PRIOR APPLICATION NUMBER: 62/776,759
 ? PRIOR FILING DATE: 2001-01-16
 ? NUMBER OF SEQ ID NOS: 11006
 ? SOFTWARE: Vectorway Fit 2.0, Seqman, ClustalX, Gaps 1.1
 ? SEQ ID NO 89794
 ? LENGTH: 25
 ? TYPE: DNA
 ? ORGANISM: Homo sapien
 ? US-10-098-263B 89794
 Query Match 60.8%, Score 15.2, EB 15, Length 25
 Best Local Similarity 60.8%, Seed No. 4, E=0.002
 Matches 17, Conservative 3, Mismatches 3, Indels 0, Gaps 0
 CY 1 CTTGAGGCGCAAGATG 20
 DB |||||||||
 24 CTTGAGGCGCAAGATG 20

GENERAL INFORMATION:
 ? APPLICANT: Miltman, Michael
 ? TITLE OF INVENTION: Human Microarray
 ? FILE REFERENCE: 3118-1
 ? CURRENT APPLICATION NUMBER: US/10/098,263B
 ? CURRENT FILING DATE: 2001-01-30
 ? PRIOR APPLICATION NUMBER: 62/776,759
 ? PRIOR FILING DATE: 2001-01-16
 ? NUMBER OF SEQ ID NOS: 11006
 ? SOFTWARE: Vectorway Fit 2.0, Seqman, ClustalX, Gaps 1.1
 ? SEQ ID NO 30412
 ? LENGTH: 25
 ? TYPE: DNA
 ? ORGANISM: Homo sapien
 ? US-10-098-263B-90412
 Query Match 60.8%, Score 15.2, EB 15, Length 25
 Best Local Similarity 60.8%, Seed No. 4, E=0.002
 Matches 17, Conservative 3, Mismatches 3, Indels 0, Gaps 0
 CY 1 CTTGAGGCGCAAGATG 20
 DB |||||||||
 24 CTTGAGGCGCAAGATG 20
 RESULT 3
 US-09-771-933-5/C
 ? Sequence 9, Application US/09771933
 ? Publication No. US2003093347A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Gill-Garrison, Rosalynn D
 ? APPLICANT: Martin, Christopher J
 ? APPLICANT: Sanchez-Felix, Manuel V
 ? TITLE OF INVENTION: Factors for decreasing lifestyle risk
 ? FILE REFERENCE: 620-130
 ? CURRENT APPLICATION NUMBER: US/09/771,933
 ? CURRENT FILING DATE: 2001-01-30
 ? NUMBER OF SEQ ID NOS: 205
 ? SOFTWARE: Patent In Ver. 2.1
 ? SEQ ID NO 5
 ? LENGTH: 25
 ? TYPE: DNA
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Description of Artificial Sequence
 ? US-09-771-933-5
 Query Match 57.6%, Score 14.4, EB 14, Length 25
 Best Local Similarity 57.6%, Seed No. 4, E=0.003
 Matches 19, Conservative 6, Mismatches 3, Indels 0, Gaps 0
 CY 1 CTTGAGGCGCAAGATG 24
 DB |||||||||
 24 CTTGAGGCGCAAGATG 24
 RESULT 4
 US-09-771-933-6
 ? Sequence 9, Application US/09771933
 ? Publication No. US2003093347A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Gill-Garrison, Rosalynn D
 ? APPLICANT: Martin, Christopher J
 ? APPLICANT: Sanchez-Felix, Manuel V
 ? TITLE OF INVENTION: Factors for decreasing lifestyle risk
 ? FILE REFERENCE: 620-130
 ? CURRENT APPLICATION NUMBER: US/09/771,933
 ? CURRENT FILING DATE: 2001-01-30
 ? NUMBER OF SEQ ID NOS: 205
 ? SOFTWARE: Patent In Ver. 2.1

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US-09-313-932-24

Query Match 48.8%; Score 12.2; DB 4; Length 20;
 Best Local Similarity 82.4%; Pred. No. 2.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 CCGAGAAAGATGAGCTC 25
 |||||
 CB 4 CCGAGATAGATGGGCTC 20

RESULT 40

US-09-313-932-93

? Sequence 93, Application US/09313932A
 ? Patent No. 6228642
 ? GENERAL INFORMATION:
 ? APPLICANT: Baker, Brenda
 ? APPLICANT: Bennett, C. Frank
 ? APPLICANT: Butler, Madeline M.
 ? APPLICANT: Shannah, William R.
 ? TITLE OF INVENTION: ANTISENSE-9413-NUCLEOTIDE MUTATION OF THE-
 ? FILE REFERENCE: ISPH-0356
 ? CURRENT APPLICATION NUMBER: US/09/313,932A
 ? CURRENT FILING DATE: 1999-05-18
 ? NUMBER OF SEQ ID NOS: 501
 ? SEQ ID NO 93
 ? LENGTH: 20
 ? TYPE: DNA
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Synthetic
 US-09-313-932-93

Query Match 48.8%; Score 12.2; DB 4; Length 20;
 Best Local Similarity 82.4%; Pred. No. 2.7e+03;
 Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 CCGAGAAAGATGAGCTC 25
 |||||
 CB 1 CCGAGATAGATGGGCTC 17

Search completed: July 21, 2003, 15:49:21
 Job time : 26.1617 secs

FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME, FIRM, FARED FAY
 REGISTRATION NUMBER: 14,950
 REFERENCE/DOCKET NUMBER: 01, 1229
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 302-993-7000
 TELEFAX: 302-773-0164
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOTIF TYPE: other nucleic acid
 DESCRIPTION: /desc = "primer"
 HYDROTHERMAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 INDIVIDUAL ISOLATE: 5' E. coli DS primer
 US-09-094-148-3

Query Match 13.8% Score 12.21 DB 3 Length 34
 Best Local Similarity 52.4% Freq NO: 2.7e+03
 Matches 10, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 CGTCCGAGCCCAAGATGAG 23
 DB 23 CGTCCGAGCCCAAGATGAG 23

RESULT 36
 US-09-167-109-38/6
 Sequence 38, Application US/09010938
 Patent No. 6392097
 GENERAL INFORMATION:
 APPLICANT: Baker, Brenda F.
 APPLICANT: Cozzelli, Lex M.
 APPLICANT: Monia, Brett P.
 APPLICANT: Xu, Xiaohong S.
 TITLE OF INVENTION: ANTISENSE MODULATION OF TGF EXPRESSION
 FILE REFERENCE: ISPH-0321
 CURRENT AFFILIATION NUMBER: 00/00000000
 CURRENT FILING DATE: 1998-10-05
 NUMBER OF SEQ ID NOS: 20
 SEQ ID NO 38
 LENGTH: 18
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: antisense sequence
 US-09-167-109-38

Query Match 13.8% Score 12.21 DB 3 Length 18
 Best Local Similarity 92.4% Freq NO: 2.7e+03
 Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 1 CGTCCGAGCCCAAGATG 17
 DB 18 CGTCCGAGCCCAAGATG 2

RESULT 37
 US-09-166-186-24
 Sequence 24, Application US/090116624
 Patent No. 6391920
 GENERAL INFORMATION:
 APPLICANT: Baker, Brenda
 APPLICANT: Bennett, C. Frank
 APPLICANT: Butler, Madeline M.
 APPLICANT: Shanahan, William R.
 TITLE OF INVENTION: ANTISENSE MODULATION OF TGF EXPRESSION

FILE REFERENCE: ISPH-0322
 CURRENT AFFILIATION NUMBER: 00/00000000
 CURRENT FILING DATE: 1998-10-05
 NUMBER OF SEQ ID NOS: 250
 SEQ ID NO 24
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: antisense sequence
 US-09-166-186-24

Query Match 48.8% Score 12.21 DB 3 Length 20
 Best Local Similarity 52.4% Freq NO: 2.7e+03
 Matches 14, Conservative 0, Mismatches 3, Indels 0, Gaps 0

QY 5 CCGAGAGATGAGCTC 25
 DB 4 CCGAGAGATGAGCTC 20

RESULT 38
 US-09-166-186-93
 Sequence 93, Application US/090116693
 Patent No. 6060580
 GENERAL INFORMATION:
 APPLICANT: Baker, Brenda
 APPLICANT: Bennett, C. Frank
 APPLICANT: Butler, Madeline M.
 APPLICANT: Shanahan, William R.
 TITLE OF INVENTION: ANTISENSE MODULATION OF TGF EXPRESSION
 FILE REFERENCE: ISPH-0322
 CURRENT AFFILIATION NUMBER: 00/00000000
 CURRENT FILING DATE: 1998-10-05
 NUMBER OF SEQ ID NOS: 250
 SEQ ID NO 93
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: antisense sequence
 US-09-166-186-93

Query Match 48.8% Score 12.21 DB 3 Length 20
 Best Local Similarity 52.4% Freq NO: 2.7e+03
 Matches 11, Conservative 0, Mismatches 3, Indels 0, Gaps 0

QY 9 CCGAGAGATGAGCTC 25
 DB 1 CCGAGAGATGAGCTC 17

RESULT 39
 US-09-313-932-24
 Sequence 24, Application US/090139224
 Patent No. 6392544
 GENERAL INFORMATION:
 APPLICANT: Baker, Brenda
 APPLICANT: Bennett, C. Frank
 APPLICANT: Butler, Madeline M.
 APPLICANT: Shanahan, William R.
 TITLE OF INVENTION: ANTISENSE MODULATION OF TGF EXPRESSION
 FILE REFERENCE: ISPH-0356
 CURRENT AFFILIATION NUMBER: 00/00000000
 CURRENT FILING DATE: 1999-01-18
 NUMBER OF SEQ ID NOS: 501
 SEQ ID NO 24
 LENGTH: 20
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: synthetic

SOFTWARE: Patent in place #1.0, Version #1.20
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/743,357
 FILING DATE: 21-Aug-1991
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: PCT/CA/90/0462
 FILING DATE: 23-FEB-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Gale, Edwin J.
 REGISTRATION NUMBER: 29,594
 REFERENCE TO PRT NUMBER: 17741
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (613) 237-6909
 TELEFAX: (613) 237-0045
 INFORMATION FOR SEQ. ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHEetical: NO
 ANTI-SENSE: NO
 US-07-43187-13

Query Match 49.6% Score 12.4 Length 32
 Best Local Similarity 22.1% Pct ID 37%
 Matches 16: Conservative 0 Mismatches 6 Indels 0 Gaps 0

CY 3 TCGAGGCCAGAGATGAGCT 24
 DB 27 TCGAGGCCAGAGATGAGCT 6

RESULT 31
 US-08-481-793-37
 Sequence 37: Application 06/06/94/793
 Patent No. 5840477
 GENERAL INFORMATION:
 APPLICANT: SEIDMAN, C.E. ET AL
 TITLE OF INVENTION: METHOD FOR DETECTING MUTATIONS ASSOCIATED WITH
 TITLE OF INVENTION: HYPERTROPHIC CARDIOMYOPATHY
 NUMBER OF SEQUENCES: 48
 ADDRESS/AGENT ADDRESS:
 ADDRESS: LAMIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 TELEFAX: (617) 227-5941
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: ETC/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/481,793
 FILING DATE: 07-Jun-1997
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 06/354,326
 FILING DATE: 12-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: HANLEY, ELIZABETH A.
 REGISTRATION NUMBER: 33,505
 REFERENCE/DOCKET NUMBER: 101-037
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7409
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ. ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 base pairs

TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..12
 US-08-481-793-37

Query Match 49.6% Score 12.4 DB 2 Length 32
 Best Local Similarity 22.0% Pct ID 37%
 Matches 16: Conservative 0 Mismatches 6 Indels 0 Gaps 0

CY 11 CAGAAATATGAGCT 24
 DB 1 CAGAAATATGAGCT 14

RESULT 32
 US-08-354-326-37
 Sequence 37: Application 06/06/94/326
 Patent No. 5842121
 GENERAL INFORMATION:
 APPLICANT: SEIDMAN, C.E. ET AL
 TITLE OF INVENTION: METHOD FOR DETECTING MUTATIONS ASSOCIATED WITH
 TITLE OF INVENTION: HYPERTROPHIC CARDIOMYOPATHY
 NUMBER OF SEQUENCES: 48
 ADDRESS/AGENT ADDRESS:
 ADDRESS: LAMIVE & COCKFIELD
 STREET: 60 State Street, suite 510
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02109-1875
 TELEFAX: (617) 227-7409
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: ASCII text
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/354,326
 FILING DATE: 01-Jun-1994
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HANLEY, ELIZABETH A.
 REGISTRATION NUMBER: 33,505
 REFERENCE/DOCKET NUMBER: 101-037
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 227-7409
 TELEFAX: (617) 227-5941
 INFORMATION FOR SEQ. ID NO: 37:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 32 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: CDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..12
 US-08-354-326-37

Query Match 49.6% Score 12.4 DB 2 Length 32
 Best Local Similarity 22.0% Pct ID 37%
 Matches 13: Conservative 1 Mismatches 1 Indels 0 Gaps 0

CY 11 CAGAAATATGAGCT 24
 DB 1 CAGAAATATGAGCT 14

RESULT 33
 PCT-US-95-07668-37

Sequence 12, Application US/09519975
Patent No. 4773582
GENERAL INFORMATION:
APPLICANT: Shin, Heng-Cheol
APPLICANT: Shin, Nam Kyu
APPLICANT: Lee, Jekyung
APPLICANT: Kaji, Shunji
TITLE OF INVENTION: THREE SEPARATE FACTOR METHODS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Shin, Heng-Cheol
STREET: Jikeung-Gaebong Apt 1014-Kos, Haeu-dong
CITY: Kwangmyung-shi
STATE: Kyungki-do
COUNTRY: Republic of Korea
ZIP: 403-060
ADDRESSEE: Shin, Nam-Kyu
STREET: #191-404 Sadang 4-dong, Dongjak-ku
CITY: Seoul
STATE:
COUNTRY: Republic of Korea
ZIP: 156-094
ADDRESSEE: Lee, Jekyung
STREET: 11/2, #102 33 Uan 4-dong, Nam-ku
CITY: Incheon
STATE:
COUNTRY: Republic of Korea
ZIP: 402-204
ADDRESSEE: Kaji, Shunji
STREET: #84 4 Doshin-dong, Seodaemut-ku
CITY: Seoul
STATE:
COUNTRY: Republic of Korea
ZIP: 120-160
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3 1/2 inch 2 0mb storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/538,875
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/94/713,300
FILING DATE:
APPLICATION NUMBER: KR 93-1751
FILING DATE: 9 FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE:
TELEFAX:
INFORMATION FOR SEQ 12 NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 27 bases
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: primer DNA
US-09-890-363-12
Query Match: 49.6% Score 12.4, DB 1, Length 27,
Post Local Similarity 72.7%, Pred. No. 2,3e+07,
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0,
QY 3 TTTGAGCCGAGAAAGATGAGT 24
TT 3 TTTGAGCCGAGAAAGATGAGT 24

RESULT 29
US-09-002-361-13
Sequence 13, Application US/09602461
Patent No. 6129516
GENERAL INFORMATION:
APPLICANT: Halling, Blair
TITLE OF INVENTION: Lipid-protein GATA bind proteins
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dechert Price & Rhoads
STREET: 401 Lewis Drive, Building 3, Suite 210
CITY: Lawrenceville
STATE: NJ
COUNTRY: USA
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEST for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/93/02,361
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEFAX: 609-520-3259
TELEX:
INFORMATION FOR SEQ 19 NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-002-361-13
Query Match: 44.4% Score 12.4, DB 4, Length 28,
Post Local Similarity 66.7%, Pred. No. 2,3e+03,
Matches 12, Conservative 4, Mismatches 2, Indels 0, Gaps 0,
QY 4 CCAGGCGCAAGAAATCA 21
UB 1 CCAGGCGCAATATATTA 18
RESULT 30
US-07-743-357-13/C
Sequence 11, Application US/07743457
Patent No. 5858646
GENERAL INFORMATION:
APPLICANT: Kang, Yong C.
TITLE OF INVENTION: Polypeptide having immunological
activity for use as diagnostic reagent
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: KIRBY EADES GALE PARKER
STREET: Box 3432, Station D
CITY: Ottawa
STATE: Ontario
COUNTRY: Canada
ZIP: K1M 1H8
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

STREET: 126 East Lincoln Avenue, P.O. Box 2089-0907

CITY: Rahway

STATE: New Jersey

COUNTRY: US

ZIP: 07065-0907

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: PC-IBM/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.0

CURRENT APPLICATION DATA

APPLICATION NUMBER: US/09/458,067

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Giessey, Joanne M.

REGISTRATION NUMBER: 32,838

REFERENCE/DOCKET NUMBER: 19457

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-4720

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

US-09-458-067-27

Query Match: 50.4% Score 12.6; DB 1; Length 29;
Best Local Similarity: 78.9%; Ident: 4; Mismatches: 4; Gaps: 0;
Matches: 15; Conservative: 0; Mismatches: 4; Ident: 4; Gaps: 0;

QY 2 GTCCGAGCCCGAAGATG 20
DB 3 GATCGAGCCCGAGTAGTG 21

RESULT 26
PCT-US96-07796-27
Sequence 27, Application PC/TUS9607795
GENERAL INFORMATION:
APPLICANT: MERCK & CO., INC.
ATTORNEY/AGENT INFORMATION:
NAME: Giessey, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19457
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-4720
TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

PCT-US96-07796-27

Query Match: 50.4% Score 12.6; DB 5; Length 29;
Best Local Similarity: 78.9%; Ident: 4; Mismatches: 4; Gaps: 0;
Matches: 15; Conservative: 0; Mismatches: 4; Ident: 4; Gaps: 0;

QY 2 GTCCGAGCCCGAAGATG 20
DB 3 GATCGAGCCCGAGTAGTG 21

RESULT 27

PCT-US96-07796-27

Sequence 27, Application PC/TUS9607795

GENERAL INFORMATION:

APPLICANT: MERCK & CO., INC.

ATTORNEY/AGENT INFORMATION:

NAME: Giessey, Joanne M.

REGISTRATION NUMBER: 32,838

REFERENCE/DOCKET NUMBER: 19457

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-4720

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

PCT-US96-07796-27

Query Match: 50.4% Score 12.6; DB 5; Length 29;
Best Local Similarity: 78.9%; Ident: 4; Mismatches: 4; Gaps: 0;
Matches: 15; Conservative: 0; Mismatches: 4; Ident: 4; Gaps: 0;

QY 2 GTCCGAGCCCGAAGATG 20
DB 3 GATCGAGCCCGAGTAGTG 21

RESULT 28

PCT-US96-07796-27

Sequence 27, Application PC/TUS9607795

GENERAL INFORMATION:

APPLICANT: MERCK & CO., INC.

ATTORNEY/AGENT INFORMATION:

NAME: Giessey, Joanne M.

REGISTRATION NUMBER: 32,838

REFERENCE/DOCKET NUMBER: 19457

TELECOMMUNICATION INFORMATION:

TELEPHONE: (908) 594-4720

TELEFAX: (908) 594-4720

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

PCT-US96-07796-27

CURRENT APPLICATION DATA:
 APPLICANT: MERCK & CO., INC.
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Gieser, Joanne M.
 REGISTRATION NUMBER: 32,848
 REFERENCE/DOCKET NUMBER: 19457
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3046
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ. NO. 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 US-09-458-067-26

Query Match 50.4%, Score 12.6, DP 1, Length 28,
 Best Local Similarity 78.9%, Prod NO. 1.8e+03,
 Matches 15, Conservative 0, Mismatches 4, Indels 0, Gaps 0.

CY 2 GTCGACGCTGACAAATG 20
 19 GACCGACGCTGACAAATG 1

RESULT 23
 PCT US-96-07796-26/C
 Sequence 27, Application 10, Filing 10, 10
 GENERAL INFORMATION:
 APPLICANT: MERCK & CO., INC.
 APPLICANT: Register, Robert B.
 APPLICANT: Shaler, Jules A.
 TITLE OF INVENTION: HERPES SIMPLEX TYPE 1 PROTEASE MUTANTS
 TITLE OF INVENTION: AND VECTORS
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ms. Joanne M. Gieser
 STREET: 126 East Lincoln Avenue, P.O. Box 2000 0707
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/07796
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Gieser, Joanne M.
 REGISTRATION NUMBER: 32,848
 REFERENCE/DOCKET NUMBER: 19457
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3046
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ. NO. 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 PCT US-96-07796-26

Query Match 50.4%, Score 12.6, DP 1, Length 28,
 Best Local Similarity 78.9%, Prod NO. 1.8e+03,
 Matches 15, Conservative 0, Mismatches 4, Indels 0, Gaps 0

CY 2 GTCGACGCTGACAAATG 20
 19 GACCGACGCTGACAAATG 1

RESULT 24
 PCT-US-96-07796-26/C
 Sequence 27, Application 10, Filing 10, 10
 GENERAL INFORMATION:
 APPLICANT: MERCK & CO., INC.
 APPLICANT: Register, Robert B.
 APPLICANT: Shaler, Jules A.
 TITLE OF INVENTION: HERPES SIMPLEX TYPE 1 PROTEASE MUTANTS
 TITLE OF INVENTION: AND VECTORS
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ms. Joanne M. Gieser
 STREET: 126 East Lincoln Avenue, P.O. Box 2000 0707
 CITY: Rahway
 STATE: New Jersey
 COUNTRY: US
 ZIP: 07065-0907
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US96/07796
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Gieser, Joanne M.
 REGISTRATION NUMBER: 32,848
 REFERENCE/DOCKET NUMBER: 19457
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 594-3046
 TELEFAX: (908) 594-4720
 INFORMATION FOR SEQ. NO. 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 HYPOTHEICAL: NO
 ANTI-SENSE: NO
 PCT-US-96-07796-26

Query Match 50.4%, Score 12.6, DP 1, Length 28,
 Best Local Similarity 78.9%, Prod NO. 1.8e+03,
 Matches 15, Conservative 0, Mismatches 4, Indels 0, Gaps 0

CY 2 GTCGACGCTGACAAATG 20
 19 GACCGACGCTGACAAATG 1

RESULT 25
 US-09-458-067-27
 Sequence 27, Application 10, Filing 10, 10
 GENERAL INFORMATION:
 PATENT NO. 5728557
 APPLICANT: Register, Robert B.
 APPLICANT: Shaler, Jules A.
 TITLE OF INVENTION: HERPES SIMPLEX TYPE 1 PROTEASE MUTANTS
 TITLE OF INVENTION: AND VECTORS
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ms. Joanne M. Gieser

COMPIER READABLE FORM:
MEDIUM TYPE: 5.25DD disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/Windows 95
SOFTWARE: Patent in Release #1.0 W
CURRENT APPLICATION DATA:
APPLICATION NUMBER US2000045225
FILING DATE
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/092,777.01
FILING DATE: 24-DEC-1996
APPLICATION NUMBER: FR 94-06643
FILING DATE: 06 MAY-1994
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: FR 93-06643
FILING DATE: 08 MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: PATCH Andrew J
REGISTRATION NUMBER: 32,925
REFERENCE/DOCET NUMBER: PFT 0094
TELECOMMUNICATION INFORMATION:

US-RUL-22
US-OR-45M-06/-26/C
Patent No. 5728557
GENERAL INFORMATION:
APPLICANT: Registrar, Robert B.
MILLICANT, Sheriff, Justice
TITLE OF INVENTION: MIXED SIMPLEX TYPE 1 ROTATED ROTANT
TITLE OF INVENTION: AND VARIANTS
NUMBER OF CO-INVENTORS: 40
CORRESPONDENCE ADDRESS:
ADDRESSER: Ms. Joanne M. Glesser
CITY: 177 East 11th Street, Apt. 4, F - E - 2000-0077
STATE: New Jersey
COUNTRY: US
ZIP: 07305-0007
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FLOPPY DISK
SOFTWARE: Mainline Release #1.0
Version #1.02

```

1 STATE: Kyungki-do
2 COUNTRY: Republic of Korea
3 ZIP: 423-060
4 ADDRESSEE: Shin, Nam-Kyu
5 STREET: #181 404 Galsang 4 Bldg, Tongjak-Ku
6 CITY: Seoul
7 STATE:
8 COUNTRY: Republic of Korea
9 ZIP: 156-094
10 ADDRESSEE: Lee, Inkyun
11 STREET: 11/2, #352 19 Duan 4 Bldg, Nam-Ku
12 CITY: Incheon
13 STATE:
14 COUNTRY: Republic of Korea
15 ZIP: 402-204
16 ADDRESSEE: Kwon, Gungwon
17 STREET: #84 4 Daeshin-dong, Seodaejeon-Ku
18 CITY: Seoul
19 STATE:
20 COUNTRY: Republic of Korea
21 ZIP: 128-198
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: Diskette 3.5inch 2.0MB storage
24 COMPUTER: IBM PC/AT
25 OPERATING SYSTEM: MS-DOS
26 SOFTWARE: Wordperfect 5.1
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: 71/088/38,876
29 FILING DATE:
30 CLASSIFICATION: 435
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 02/08/193,336
33 FILING DATE:
34 APPLICATION NUMBER: KR 93-1751
35 FILING DATE: 9-FEB-1993
36 ATTORNEY/AGENT INFORMATION:
37 NAME:
38 REGISTRATION NUMBER:
39 REFERENCE/SECRET NUMBER:
40 TELECOMMUNICATION INFORMATION:
41 TELEPHONE:
42 TELEFAX:
43 INFORMATION FOR SEQ ID NO: 57:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 22 bases
46 TYPE: Nucleic acid
47 STRANDEDNESS: single
48 TOPOLOGY: linear
49 MOLECULE TYPE: primer DNA
50 US-08-538-875-57
51 Query Match 51.2% Score 12.8; DB 1; Length 22;
52 Post Local Similarity 40.9; First N 1; 4-11;
53 Matches 14; Conservation 0; Mismatch 0; Indels 0; Gaps 0
54
55 10 CCAGACATGAGATG 25
56 18 CCAGACATGAGATG 3
57
58 RESULT 18
59 US-08-117-952-501
60 Sequence 501, Application 05/08/17952
61 Patent No. 5681760
62 GENERAL INFORMATION:
63 APPLICANT: Evans, Glen A.
64 APPLICANT: Smith, Michael W.
65 TITLE OF INVENTION: METHOD FOR SEPARATION OF SEQUENCE
66 TITLE OF INVENTION: SEPARATION OF COMPLEX GENOMES
67 NUMBER OF SEQUENCES: 797
68 CORRESPONDENCE ADDRESS:
69 ADDRESS: Preeti, Schroeder, Prueggemann & Glorv
70 STREET: 444 South Flower Street, Suite 2000

```

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1 CITY: Los Angeles
2 STATE: CA
3 COUNTRY: USA
4 ZIP: 90071
5 COMPUTER READABLE FORM:
6 MEDIUM TYPE: Floppy disk
7 COMPUTER: IBM PC compatible
8 OPERATING SYSTEM: PC-DOS/MS-DOS
9 SOFTWARE: Patent In Release #10, Version #1.25
10 CURRENT APPLICATION DATA:
11 APPLICATION NUMBER: 05/08/117,952
12 FILING DATE: 07-SEP-1993
13 CLASSIFICATION: 435
14 PRIOR APPLICATION DATA:
15 APPLICATION NUMBER: US 08/078,471
16 FILING DATE: 15-JUN-1993
17 ATTORNEY/AGENT INFORMATION:
18 NAME: Reiter, Stephen R.
19 REGISTRATION NUMBER: 31,192
20 REFERENCE/SECRET NUMBER: 041 9473
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: 619-546-4737
23 TELEFAX: 619-546-9392
24 INFORMATION FOR SEQ ID NO: 501:
25 SEQUENCE CHARACTERISTICS:
26 LENGTH: 30 base pairs
27 TYPE: nucleic acid
28 STRANDEDNESS: single
29 TOPOLOGY: linear
30 MOLECULE TYPE: Oligonucleotide
31 HYPOTHEetical: NO
32 ANTI-SENSE: NO
33 US-08-117-952-501
34 Query Match 51.4; Score 12.8; DB 2; Length 30;
35 Post Local Similarity 70.8; First N 1; 5-9;
36 Matches 17; Conservation 0; Mismatch 7; Indels 0; Gaps 0
37
38 2 GTCCAGCCGAGACATGAGATG 25
39 1 GTCCAGCCGAGACATGAGATG 10
40
41 RESULT 19
42 US-08-737-271-7
43 Sequence 7, Application 05/08/32271
44 Patent No. 5955300
45 GENERAL INFORMATION:
46 APPLICANT: FAURE, Florence
47 APPLICANT: HERCEND, Thierry
48 APPLICANT: HUARD, Bertrand
49 APPLICANT: TRIBEL, Frederic
50 TITLE OF INVENTION: METHOD FOR IDENTIFYING FEATURES OF THE
51 TITLE OF INVENTION: CAG / IS CHIN. IDENTIFICATION OF MUTATIONS
52 TITLE OF INVENTION: ANTI-IDIOTYPE ANTIBODIES
53 NUMBER OF SEQUENCES: 8
54 CORRESPONDENCE ADDRESS:
55 ADDRESS: YOUNG & THOMPSON
56 STREET: 745 South 23rd Street
57 CITY: Arlington
58 STATE: Virginia
59 COUNTRY: United States of America
60 ZIP: 22202
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Floppy disk
63 COMPUTER: IBM PC compatible
64 OPERATING SYSTEM: PC-DOS/MS-DOS
65 SOFTWARE: Patent In Release #10, Version #1.15
66 CURRENT APPLICATION DATA:
67 APPLICATION NUMBER: US/08/737,271
68 FILING DATE: 24 DEC 1996
69 CLASSIFICATION: 536
70 PRIOR APPLICATION DATA:

```

```

1  ZIR: 422-060
2  INVENTOR: NAM KYU
3  STREET: #12-424 SONG 1 RD., BONGJAE GU
4  CITY: Seoul
5  STATE:
6  COUNTRY: Republic of Korea
7  ZIR: 156-04
8  ADDRESS: Lee, Inkyung
9  STREET: 11/2, #102-39 JUNG 4 DONG, NAM KU
10 CITY: Incheon
11 STATE:
12 COUNTRY: Republic of Korea
13 ZIR: 402-204
14 ADDRESS: Kang, Sungzong
15 STREET: #24 4 SONGJIN RD., GILJANGDONG IN
16 CITY: Seoul
17 STATE:
18 COUNTRY: Republic of Korea
19 ZIR: 150-160
20 INVENTOR RELEASABLE FORM:
21 MEDIUM TYPE: Diskette 3.5inch 2.0MB storage
22 COMPUTER: Irv PC/AT
23 OPERATING SYSTEM: MS-DOS
24 SOFTWARE: Wordperfect 5.1
25 CURRENT APPLICATION DATA:
26 APPLICATION NUMBER: 92/92/332,575
27 CLASSIFICATION: 435
28 FILING DATE:
29 PILING DATE:
30 HIGH APPLICATION DATA:
31 APPLICATION NUMBER: 92/92/332,575
32 PILING DATE:
33 APPLICATION NUMBER: 92-35-1701
34 FILING DATE: 9-FEB-1993
35 ATTORNEY/AGENT INFORMATION:
36 NAME:
37 REGISTRATION NUMBER:
38 RESEARCH/INSTR. NUMBER:
39 TECHNOLOGICAL INFORMATION:
40 TELEPHONE:
41 TELEFAX:
42 INFORMATION FOR SEQ ID NO. 55:
43 SEQUENCE CHARACTERISTICS:
44 LENGTH: 22 bases
45 TYPE: nucleic acid
46 STRANDEDNESS: single
47 TOPOLOGY: linear
48 MOLECULE TYPE: primer DNA
49 ORIGIN: 5'
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
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83
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```

APPLICANT: Andrews, William H.
 TITLE OF INVENTION: Antisense Compounds for Treating and
 Title of Invention: Inhibiting Telomerase Reverse Transcriptase
 NUMBER OF SEQUENCES: 72
 CORRESPONDENCE ADDRESS:
 ADDRESS: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3814
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US 08/851,843
 FILING DATE: 31 MAR 1998
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/724,743
 FILING DATE: 01-OCT-1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/444,419
 FILING DATE: 18-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/446,817
 FILING DATE: 25-APR-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/451,843
 FILING DATE: 05-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/454,850
 FILING DATE: 09-MAY-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/411,412
 FILING DATE: 14 AUG 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/412,951
 FILING DATE: 14 AUG 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/412,103
 FILING DATE: 14-AUG-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/474,519
 FILING DATE: 19-NOV-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/774,584
 FILING DATE: 19 NOV 1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: W. 08/777,719
 FILING DATE: 01-OCT-1997
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: W. 08/777,719
 FILING DATE: 01-OCT-1997
 APPLICATION NUMBER: 42,638
 REFERENCE/BOOKLET NUMBER: 01584-00360005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0000
 INFORMATION FOR SEQ ID NO: 40:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "phosphorothioate oligonucleotide"
 US-09-890-363-5

Query Match 53.68; Score 13.4; DB 4; Length 40
 Best Local Similarity 43.38; Pval 0.00000000
 Matches 14; Conserving 0; Mismatches 11; Gaps 0
 47 6 GAGCCGAGAAATG 20
 || |||||
 13 GAGCCGAGAAATG 27
 RESULT 13
 US-08-117-952-681/C
 Sequence 681, Application us/0817952
 Patent No. 593760
 GENERAL INFORMATION:
 APPLICANT: Evans, Glen A.
 APPLICANT: Smith, Michael W.
 TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
 TITLE OF INVENTION: SAMPLING OF GENOME
 NUMBER OF SEQUENCES: 797
 CORRESPONDENCE ADDRESS:
 ADDRESS: Pretty, Schroeder, Ruggmann & Clark
 STREET: 444 South Flower Street, Suite 2000
 CITY: Los Angeles
 STATE: CA
 COUNTRY: USA
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/041,102
 FILING DATE: 07-SEP-1993
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/004,471
 FILING DATE: 15 JUN 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Pretty, Stephen B.
 REGISTRATION NUMBER: 31,192
 REFERENCE/AGENT NUMBER: 141 9423
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 619-546-4737
 TELEFAX: 619-546-9392
 INFORMATION FOR SEQ ID NO: 681:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: double
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US 08-117-952-681
 Query Match 52.94; Score 12.5; DB 4; Length 40
 Best Local Similarity 43.38; Pval 0.00000000
 Matches 15; Conserving 0; Mismatches 11; Gaps 0
 47 4 GAGCCGAGAAATG 21
 || |||||
 19 GAGCCGAGAAATG 2
 RESULT 14
 US-09-306-595C-32
 Sequence 32, Application US/09306595C
 Patent No. 6284506
 GENERAL INFORMATION:
 APPLICANT: HOSHINO, TATSUO
 APPLICANT: OGUMA, KAZUYUKI
 APPLICANT: SETOGUCHI, YUTAKA

FILING DATE: 17 MAY 1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Kenneth D. Staley
 REGISTRATION NUMBER: 31,665
 REFERENCE/DOCKET NUMBER: 5470 715
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-420-2200
 TELEFAX: 919-681-3175
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-09-446 089A 6

Query Match 53.6% Score 13.4 DB 1 Length 30
 Best Local Similarity 70.0% Seed 17
 Matches 14, Conservative 0, Mismatches 7, Indels 0, Gaps 0
 C1 1 CGTCGAGCTTGAAGATAGAGTTC 25
 C2 3 CGTGAATGGCAAGACAGAGAGG 27

RESULT 10
 US-09-327-832-8
 Sequence 8, Application US/0828584
 Patent No. 506762
 GENERAL INFORMATION:
 APPLICANT: Ono, Santa J.
 TITLE OF INVENTION: Transcription Factor Regulated Wnt
 TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
 NUMBER OF SEQUENCES: 17
 REFERENCE/DOCKET NUMBER: 1107-46362
 TELECOMMUNICATION INFORMATION:
 ADDRESS: Ramsey, Ralph, Morin & Barrett
 STREET: 1001 G Street, N.W.
 CITY: Washington, D.C.
 STATE: District of Columbia
 COUNTRY: U.S.A.
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #10, Version #1.0
 CURRENT APPLICATION DATA:
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fossolske, Lawrence H.
 REGISTRATION NUMBER: 34,698
 REFERENCE/DOCKET NUMBER: 1107-46362
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 508-9153
 TELEFAX: 202 508-9299
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: homo sapiens
 US-09-327-832-8
 Query Match 53.6% Score 13.4 DB 2 Length 30
 Best Local Similarity 70.0% Seed 17
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

Best Local Similarity 70.0% Seed 17 Length 30
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0
 C1 3 TCGAGCTTGAAGATAGAGTTC 25
 C2 5 TCGGCAAGACAGAGAGG 27

RESULT 11
 US-09-594-9
 Sequence 8, Application US/0828584
 Patent No. 506762
 GENERAL INFORMATION:
 APPLICANT: Ono, Santa J.
 TITLE OF INVENTION: Transcription Factor Regulated Wnt
 TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
 NUMBER OF SEQUENCES: 16
 REFERENCE/DOCKET NUMBER: 1107-46362
 TELECOMMUNICATION INFORMATION:
 ADDRESS: Ramsey, Ralph, Morin & Barrett
 STREET: 1001 G Street, N.W.
 CITY: Washington, D.C.
 STATE: District of Columbia
 COUNTRY: U.S.A.
 ZIP: 20001
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #10, Version #1.0
 CURRENT APPLICATION DATA:
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Fossolske, Lawrence H.
 REGISTRATION NUMBER: 34,698
 REFERENCE/DOCKET NUMBER: 1107-46362
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 508-9153
 TELEFAX: 202 508-9299
 INFORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: homo sapiens
 US-09-594-9

Query Match 53.6% Score 13.4 DB 2 Length 30
 Best Local Similarity 70.0% Seed 17
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0
 C1 3 TCGAGCTTGAAGATAGAGTTC 25
 C2 5 TCGGCAAGACAGAGAGG 27


```

US-08-442-134A-6
Sequence 6, Application US/08442134A
Patent No. 5696088
GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harder, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: RNA Encoding the Human F20 Receptor and
TITLE OF INVENTION: Nalt Cells Expressing F20 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Selitzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NC 28234
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
FILING DATE: 16 MAY 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/COCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 429 2000
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-442-134A-6

Query Match 53.0% Score 13.4, DB:1, Length 30,
Best Local Similarity 56.0% Freq. No. 7, 6e+02
Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0
1 GCTGCAATGCAAAATGATGCTG 25
2 CTTGSAATGCAAAATGATGCTG 27
3 CTTGSAATGCAAAATGATGCTG 27

RESULT 9
US-08-444-081B-6
Sequence 6, Application US/08444081B
Patent No. 5697816
GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harder, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: RNA Encoding the Human F20 Receptor and
TITLE OF INVENTION: Nalt Cells Expressing F20 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Selitzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NC 28234
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
FILING DATE: 16 MAY 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/COCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 429 2000
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-444-081B-6

```

```

ADDRESS: Bell, Selitzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NC 28234
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
FILING DATE: 16 MAY 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/COCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 429 2000
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-444-081B-6

Query Match 53.0% Score 13.4, DB:1, Length 30,
Best Local Similarity 56.0% Freq. No. 7, 6e+02
Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0
1 GCTGCAATGCAAAATGATGCTG 25
2 CTTGSAATGCAAAATGATGCTG 27
3 CTTGSAATGCAAAATGATGCTG 27

RESULT 9
US-08-446-088A-6
Sequence 6, Application US/08446088A
Patent No. 5691156
GENERAL INFORMATION:
APPLICANT: Boucher, Richard C.
APPLICANT: Weisman, Gary A.
APPLICANT: Turner, John T.
APPLICANT: Harder, Thomas K.
APPLICANT: Parr, Claude E.
APPLICANT: Sullivan, Daniel M.
APPLICANT: Erb, Laura
APPLICANT: Lustig, Kevin D.
TITLE OF INVENTION: RNA Encoding the Human F20 Receptor and
TITLE OF INVENTION: Nalt Cells Expressing F20 Receptors
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Selitzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: NC 28234
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.0
CURRENT APPLICATION DATA:
FILING DATE: 16 MAY 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/COCKET NUMBER: 5470-71A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919 429 2000
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-446-088A-6

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      1 APPLICATION NUMBER: US980627-0330
      2 FILING DATE
      3 PUBLICATION DATA:
      4 PUBLICATION NUMBER: US 58/294,290
      5 FILING DATE: 29 JULY 94
      6 PRIOR APPLICATION DATA:
      7 APPLICATION NUMBER: US 58/039,212
      8 FILING DATE: 30 MAY 94
      9 PRIOR APPLICATION DATA:
     10 APPLICATION NUMBER: US 58/121,438
     11 FILING DATE: 14 SEP 1993
     12 PRIOR APPLICATION DATA:
     13 APPLICATION NUMBER: US 57/746,232
     14 FILING DATE: 14 SEP 1992
     15 ATTORNEY/AGENT INFORMATION:
     16 NAME: Myers, Paul L.
     17 REGISTRATION NUMBER: 37695
     18 REFERENCE/CITATION NUMBER: R&B 02/PQ
     19 TELECOMMUNICATIONS INFORMATION:
     20 TELEPHONE: (617)227-5941
     21 TELEFAX: (617)227-5941
     22 INFORMATION FOR SEQ ID NOS: 1-1:
     23 SEQUENCE CHARACTERISTICS:
     24 LENGTH: 24 base pairs
     25 TYPE: nucleic acid
     26 STRANDEDNESS: single
     27 TOPOLOGY: linear
     28 MOLECULE TYPE: cDNA
     29 POT-0595-09345-19
    300
Query Match          55.3%, Score 13.8; DB 5; Length 24;
                        E-value 59.27; Filt: Not Filtered;
Matched 15, Mismatched 9, Mismatch 27, Indels 0, Gaps 0
CY       1 CCGGAGACCCGGAAG 17
        | |||||
EB       5 CTTTGGCTTAAAG 21

RESULT 6
US-09-452-e24A-10
Sequence 10; Application US/99452e24A
Patent No. 642895
GENERAL INFORMATION:
APPLICANT: BREMER, Jonathan S.
ATTORNEY: Ding, Yao Zhong
ARTICL ANT: Am, Li Hai
TITLE OF INVENTION: IMMUNOSUPPRESSIVE AND IMMUNOSTIMULATORY COMPOSITIONS
FIELD OF INVENTION: DEFINITION OF IL-10
FILE REFERENCE: UMC0103622
CURRENT APPLICATION NUMBER: US 09/452-e24A
CURRENT FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 10
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Definition of Artificial Sequence Symbolic
OTHER INFORMATION: Primer
US-09-452-e24A-10
Query Match          54.6%; Score 13.4; DB 4; Length 24;
                        Best Local Similarity 93.3%; Filt: Not Filtered;
Matches 14, Conservative 0, Mismatches 10, Indels 0, Gaps 0
CY       10 CCGAAGAATGAGT 24
         |||||||
EB       4 CCGAAGAATGAGT 18

```

```

C 977 10 40.0 26 1 US-08-416-241-42 Sequence 35, Appl
C 978 10 40.0 26 2 US-08-416-273-35 Sequence 35, Appl
C 979 10 40.0 26 3 US-08-416-122-17 Sequence 17, Appl
C 980 10 40.0 26 4 US-02-119-024-35 Sequence 35, Appl
C 981 10 40.0 26 5 US-08-416-494-4 Sequence 4, Appl
C 982 10 40.0 26 6 US-08-417-226-35 Sequence 24, Appl
C 983 10 40.0 26 7 US-08-416-476-74 Sequence 35, Appl
C 984 10 40.0 26 8 US-08-196-131-35 Sequence 35, Appl
C 985 10 40.0 26 9 US-08-643-732-35 Sequence 35, Appl
C 986 10 40.0 26 10 US-08-416-494-4 Sequence 4, Appl
C 987 10 40.0 27 1 US-08-409-409-12 Sequence 12, Appl
C 988 10 40.0 27 2 US-07-977-084A-255 Sequence 25, Appl
C 989 10 40.0 27 3 US-08-143-219-20 Sequence 20, Appl
C 990 10 40.0 27 4 US-08-416-246A-46 Sequence 34, Appl
C 991 10 40.0 27 5 US-08-292-597-58 Sequence 58, Appl
C 992 10 40.0 27 6 US-08-344-653-58 Sequence 58, Appl
C 993 10 40.0 27 7 US-08-473-685-58 Sequence 58, Appl
C 994 10 40.0 27 8 US-08-356-426P-255 Sequence 25, Appl
C 995 10 40.0 27 9 US-08-483-888-58 Sequence 58, Appl
C 996 10 40.0 27 10 US-08-416-494-4 Sequence 4, Appl
C 997 10 40.0 27 11 US-08-411-944-25 Sequence 25, Appl
C 998 10 40.0 27 12 US-08-157-753-58 Sequence 58, Appl
C 999 10 40.0 27 13 US-09-157-230-58 Sequence 58, Appl
1000 10 40.0 27 14 US-08-587-611-58 Sequence 58, Appl

```

ALIGNMENTS

```

RESULT 1
US-09-489-765A-31/2
Sequence 31, Application US/09489765A
Patent No. 6121029
GENERAL INFORMATION:
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: Artificially Modified Mammalian Cell Lines for Synthesis of RNA
FILE REFERENCE: R10-0124
CURRENT APPLICATION NUMBER: US/09/489-765A
CURRENT FILING DATE: 2000-01-13
NUMBER OF SEQ ID NOS: 85
SEQ ID NO 31
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-09-489-765A-31

```

```

Query Match 55.0% Score 14, DB 4, Length 23
Best Local Similarity 100.0%, Freq. No. 1, 100.0%
Matches 14, Conservative 0, Mismatches 0, Indels 0, Gaps 0
DB 16 AAAAAATGATGATG 3

```

```

RESULT 2
US-09-489-765A-32/2
Sequence 32, Application US/09489765A
Patent No. 6121029
GENERAL INFORMATION:
APPLICANT: Madeline M. Butler
APPLICANT: Robert McKay
APPLICANT: Brett P. Monia
APPLICANT: Jacqueline Wyatt
TITLE OF INVENTION: Artificially Modified Mammalian Cell Lines for Synthesis of RNA
FILE REFERENCE: R10-0124
CURRENT APPLICATION NUMBER: US/09/489-765A
CURRENT FILING DATE: 2000-01-13

```

```

NUMBER OF SEQ ID NOS: 85
SEQ ID NO 32
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-09-489-765A-32

```

```

Query Match 56.0% Score 14, DB 4, Length 20
Best Local Similarity 100.0%, Freq. No. 3, 66.0%
Matches 14, Conservative 0, Mismatches 1, Indels 0, Gaps 0
DB 17 AAAAAATGATGATG 25
DB 20 AAAAAATGATGATG 7

```

```

RESULT 3
US-08-707-743-11
Sequence 11, Application US/0807743
Patent No. 6063983
GENERAL INFORMATION:
APPLICANT: George J. Kalos, Kalia
TITLE OF INVENTION: Methods and Apparatus for the Synthesis of RNA
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: 14
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/707,743
FILING DATE:
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 68/083,225
FILING DATE: 05-SEPT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,365
REFERENCE/DOCKET NUMBER: MGP-036CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-707-743-11

```

```

Query Match 55.2% Score 13.8, DB 3, Length 24
Best Local Similarity 88.2%, Freq. No. 4, 76.0%
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0
DB 1 CGTCCGAGCCGAGAAAG 17
DB 5 CGTCCGAGCCGAGAAAG 21

```

```

RESULT 4
US-08-243-400A-19
Sequence 19, Application US/080824300A
Patent No. 6122378

```


[illegible]




```

Best local similarity: 100.0%, From: Max: 130.0%
Matches: 13; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
QY 11 CAGAAAGATGAGG 23
   |||||
DB 13 CAGAAAGATGAGG 1

RESULT 38
AAQ24564
ID AAQ24564 standard; DNA; 29 BP.
XX
AC AAQ24564;
XX
DT 26 NOV-1992 (first entry)
XX
DE NANBH peptide A primer 2.
XX
KM Beta (3') expressing vector; polynucleotide chain (antigen; antigen;
XX PCR; antibody; peptide B, ss.
XX
OS Non A, non B hepatitis virus.
XX
PN JP04121193 A.
XX
PD 22-APR-1992.
XX
PE 07 SEP-1992 900P 0218112.
XX
PF 07 SEP-1992 100P 0218112.
XX
PA (KANA) KANAKI (KANA) KANAKI (KANA) KANAKI
XX
DB WPI; 1992 188068673
XX
PT New non A, non B hepatitis virus fused peptide - useful as
XX antibody assay reagent for NANBH as it retains both
XX antigenicities and increases detection percentage.
XX
PS (synthetic) 113 5' 111P 188068673.
XX
CC The sequence from the AAQ24564 A and B regions which are used to
XX amplify the DNA which encodes peptide A from the non-A, non-B
XX hepatitis virus (NANBH) (see also AAQ24564) Peptide A can be fused
XX to peptide B (see also AAQ24564) to form the DNA encoding a novel
XX peptide (see also AAQ24564). This novel peptide can be linked to a
XX carrier molecule, e.g. a beta gal. The novel peptide-beta gal fusion
XX retains the antigenicity of both components and can be used in the
XX detection of NANBH. The DNA encoding the novel peptide can be
XX integrated into a vector to express a gene and this can be used to
XX transform a host cell which can be cultured to express the peptide.
XX This novel peptide can be used as an antigen in an assay method to
XX detect NANBH antibody.
XX
SQ Sequence 29 BP; 6 A; 10 C; 12 G; 1 T; 1 other;
QY Query Match 52.0%; Score 13; DB 13; Length 29;
Best local similarity: 76.2%; From: 130.04;
Matches: 16; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;
QY 3 TCGACGCTGAGAAATGAGG 23
   |||||
DB 2 TCGACGCTGAGAAATGAGG 22

RESULT 39
AAV26169
ID AAV26169 standard; DNA; 33 BP.
XX
AC AAV26169;
XX
DT 24 JUL-1998 (first entry)
XX

```

```

XX
XX Best local similarity: 100.0%, From: Max: 130.0%
XX Matches: 13; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;
XX QY 11 CAGAAAGATGAGG 23
XX   |||||
XX DB 13 CAGAAAGATGAGG 1
XX
XX RESULT 38
XX AAQ24564
XX ID AAQ24564 standard; DNA; 29 BP.
XX XX
XX AC AAQ24564;
XX XX
XX DT 26 NOV-1992 (first entry)
XX XX
XX DE NANBH peptide A primer 2.
XX XX
XX KM Beta (3') expressing vector; polynucleotide chain (antigen; antigen;
XX XX PCR; antibody; peptide B, ss.
XX XX
XX OS Non A, non B hepatitis virus.
XX XX
XX PN JP04121193 A.
XX XX
XX PD 22-APR-1992.
XX XX
XX PE 07 SEP-1992 900P 0218112.
XX XX
XX PF 07 SEP-1992 100P 0218112.
XX XX
XX PA (KANA) KANAKI (KANA) KANAKI (KANA) KANAKI
XX XX
XX DB WPI; 1992 188068673
XX XX
XX PT New non A, non B hepatitis virus fused peptide - useful as
XX XX antibody assay reagent for NANBH as it retains both
XX XX antigenicities and increases detection percentage.
XX XX
XX PS (synthetic) 113 5' 111P 188068673.
XX XX
XX CC The sequence from the AAQ24564 A and B regions which are used to
XX XX amplify the DNA which encodes peptide A from the non-A, non-B
XX XX hepatitis virus (NANBH) (see also AAQ24564) Peptide A can be fused
XX XX to peptide B (see also AAQ24564) to form the DNA encoding a novel
XX XX peptide (see also AAQ24564). This novel peptide can be linked to a
XX XX carrier molecule, e.g. a beta gal. The novel peptide-beta gal fusion
XX XX retains the antigenicity of both components and can be used in the
XX XX detection of NANBH. The DNA encoding the novel peptide can be
XX XX integrated into a vector to express a gene and this can be used to
XX XX transform a host cell which can be cultured to express the peptide.
XX XX This novel peptide can be used as an antigen in an assay method to
XX XX detect NANBH antibody.
XX XX
XX SQ Sequence 29 BP; 6 A; 10 C; 12 G; 1 T; 1 other;
XX
XX QY Query Match 52.0%; Score 13; DB 13; Length 29;
XX Best local similarity: 76.2%; From: 130.04;
XX Matches: 16; Conservative: 0; Mismatches: 5; Indels: 0; Gaps: 0;
XX QY 3 TCGACGCTGAGAAATGAGG 23
XX   |||||
XX DB 2 TCGACGCTGAGAAATGAGG 22
XX
XX RESULT 39
XX AAV26169
XX ID AAV26169 standard; DNA; 33 BP.
XX XX
XX AC AAV26169;
XX XX
XX DT 28-SEP-2000 (first entry)
XX XX
XX DE PCR primer, StructBsp1201.
XX XX
XX KM Antigen presentation; vaccine; infectious disease; antibody; antibody;
XX KM molecular scaffold; immune response; farm animal; organism;
XX KM immunostimulatory; cytotoxic; antibody; PCR primer;
XX KM JUN leucine zipper; ss.
XX XX
XX OS Sindbis virus.
XX

```


CC to span larger of variable gaps, and a greater number of gaps, between
CC DNA binding substrates. Sequences AA43348-357 represent PCR primers
CC used in the course of the invention.

CC Sequence 15 Ref: 4 A: 8 G: 9 G: 14 T: 0 Other:

Query Match: 52.8%, Score 12.0, E-02, Length 35;

Best Local Similarity: 83.3%, Fred. No. 1.1e-04;

Matches: 16; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

CC 5 CGAGCCGACAGATGAGTGC 25

DB 18 CATCTCTAAAAAATACCG 1

RESULT 14
AA772379

ID AA772379 standard; DNA: 21 BP.

XX AA772379,

DT 10 SEP-2001 (first entry)

DE Human biallelic marker upstream amplification primer SEQ ID No. 6735

KM Human genome; biallelic marker; high density disequilibrium map;

KM genomic map; haplotype; phenotype; polymorphic base; genotyping;

KM haplotype; hybridization; identification; characterization;

KM left allele; right allele; left polymorphic base; PCR primer;

OS diagnosis; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

Best Local Similarity: 76.2%, Fred. No. 1.2e-04;
Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

CC 5 CGAGCCGACAGATGAGTGC 25

DB 21 CAGGACCGATTAATATAGTGC 1

RESULT 15
ABN11989

ID ABN11989 standard; DNA: 25 BP.

XX ABN11989;

DT 29 MAY-2002 (first entry)

DE Human GEMF-1 cDNA scanning SEQ ID No. 6 sequence SEQ ID No. 11601

KM Human; genome-derived myosin-like protein; GEMF-1; hGEMF-1; hGEMF-1;

KM muscle; myosin; cDNA; cDNA; cDNA; cDNA; cDNA; cDNA; cDNA; cDNA;

KM skeletal muscle disorder; aplasia; scleroderma; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

Best Local Similarity: 76.2%, Fred. No. 1.2e-04;
Matches: 16; Conservative: 0; Mismatches: 0; Indels: 0; Gaps: 0;

CC 5 CGAGCCGACAGATGAGTGC 25

DB 21 CAGGACCGATTAATATAGTGC 1

RESULT 15
ABN11989

ID ABN11989 standard; DNA: 25 BP.

XX ABN11989;

DT 29 MAY-2002 (first entry)

DE Human GEMF-1 cDNA scanning SEQ ID No. 6 sequence SEQ ID No. 11601

KM Human; genome-derived myosin-like protein; GEMF-1; hGEMF-1; hGEMF-1;

KM muscle; myosin; cDNA; cDNA; cDNA; cDNA; cDNA; cDNA; cDNA; cDNA;

KM skeletal muscle disorder; aplasia; scleroderma; ss.

OS Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

XX Homo sapiens.

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XX Homo sapiens.

```

FH 07-APR-2000; LOCUS ID#16181;
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Lehmann-Bruhnsma K, Liaw CW, Lin J;
XX
XX WPI; 2001-64979/74
XX
XX Identifying agents of G protein-coupled receptors (GPCRs) for use in
XX disease treatment; computer program containing various segments with
XX versions of GPCRS -
XX
XX Example 2; Page 53; Paper English.
XX
XX The invention relates to G protein-coupled receptors (GPCRs) for which
XX the end-points listed have been identified. Nucleic acids are
XX constitutively produced variants of known GPCR are used in the
XX invention for the direct identification of end-point sequences as
XX receptor ligands, inverse agonists or partial agonists. Such
XX agonists are useful as therapeutic agents for diseases or disorders
XX associated with GPCRs. The present sequence is a primer used for
XX site-directed mutagenesis of known GPCR (a known GPCR) in an example
XX illustrating the invention.
XX
XX Sequence 31 BF, 2 A, 7 C, 10 G, 12 T, 6 other;
XX
XX Query Match 52.8%; Score 19.2; E=0.2; Length 21;
XX Best Local Similarity 83.3%; Pctd No. 110045;
XX Matched 15; Characterized 2; Window Size 1; Subst. Q; Gap
XX
XX 4 CGAGCGGCAAAAGTGAAT 31
XX ||||| |||||
XX DB 31 CGCAGTCACCAAAAGTGA 14
XX
XX RESULT 32
XX AB197920
XX ID AB197920 standard; DNA; 31 BF;
XX
XX AB197920;
XX
XX 18-FEB-2002 first entry
XX
XX Non-subjected human effect receptor variant; amino acid H 200-202
XX
XX Homo sapiens.
XX
XX Synaptic
XX
XX M020617712 AZ;
XX
XX 18-OCT-2001;
XX
XX 05-APR-2001; 2001W0001000
XX
XX 07 APR-2000; 2000JUS-195747P;
XX
XX (AREN-) ARENA PHARM INC.
XX
XX Lehmann-Bruhnsma K, Liaw CW, Lin J;
XX
XX WPI; 2001-64979/74.
XX
XX Identifying agents of G protein-coupled receptors (GPCRs) for use in
XX disease treatment; computer program containing various segments with
XX versions of GPCRS -
XX
XX Example 2; page 59; paper English.
XX
XX The invention relates to G protein-coupled receptors (GPCRs) for which

```

[illegible]

PF 08 FEB 2001; 2001WO-US04130.
 XX
 XX 08 FEB 2001; 2000US-0181039.
 XX
 XX (GENA) GENAISCANCE PHARM INC.
 XX
 XX Anastasio AE, Chow A, Denton SR, Nardabian K, Stephens JC,
 XX
 XX WPI; 2001-522460/57.
 XX
 XX Novel polynucleotide containing one of 11, F01 F011, single nucleotide
 XX polymorphisms in human interleukin-15 gene, and useful for treating
 XX disorders affected by expression of function of interleukin-15 isogene
 XX
 XX Example 1, Page 28, 29pp; English.
 XX
 XX The present invention is a PCR primer useful for amplifying human
 XX interleukin-15 (IL-15) gene fragment. IL-15 gene is located on
 XX chromosome 4p13. The polymorphic variants of IL-15 genes are useful
 XX for studying the expression and function of IL-15 genes and expressing
 XX IL-15 protein for use in useful for screening for candidate drugs to
 XX treat diseases related to IL-15 activity. Genotyping of haplotype in
 XX individual at the novel IL-15 polymorphic sites are useful for studying
 XX polymorphism diversity, anthropological lineage, the significance of
 XX diversity and lineage of the phenotypic level, paternity testing,
 XX forensic applications and for identifying associated between IL-15
 XX genetic variations and a trait such as level of drug response or
 XX susceptibility to disease. Genotyping an individual between a genotype
 XX of haplotype of IL-15 gene is useful for developing diagnostic tests and
 XX therapeutic treatments for infectious, human immunodeficiency virus and
 XX T-cell leukemia. The identification of an association between a clinical
 XX response and a genotype or haplotype for haplotype panel for the IL-15
 XX gene may be the basis for designing a diagnostic method to determine
 XX these individuals who will or will not respond to the treatment, or
 XX alternatively, will respond at a lower level and thus may require more
 XX treatment, i.e., a greater dose of a drug. The genotyping of haplotype
 XX methods are also useful for developing drugs targeting IL-15. The
 XX genotyping and haplotype methods are also useful in designing clinical
 XX trials. IL-15 RNA is useful for therapeutic purposes for treating
 XX disorders affected by expression of function of novel IL-15 isogene and
 XX also in gene therapy. Expression of IL-15 gene may be induced off
 XX by transfecting a targeted cell, tissue or cell population of an
 XX organism with a vector expressing high levels of recombinable mRNA for
 XX the isogene.
 XX
 XX Sequence 21 BP; 5 A; 7 C; 6 G; 5 T; 0 other;
 XX
 XX Query Match 52.8%; Score 13.2; DB 22; Length 23;
 XX Best local similarity 83.3%; Pred. No. 1e+04;
 XX Matches 15; Conservation 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 9 GCGGCGAAGAAATGACATTC 25
 XX ||||| ||||| |||||
 XX 23 GCGGCAACGAGATGATTC 6
 XX
 XX RESULT 30
 XX AAST18161
 XX ID AAST18161 standard; DNA; 24 BP.
 XX
 XX AA191919;
 XX
 XX 26 MAR 2002 (first entry)
 XX
 XX CERP TaqII polymorphism detection PCR primer #1.
 XX
 XX Carbohydrate disease, TqII polymorphism, family heart disease, SC,
 XX cholesteryl ester transfer protein, CERP, Taq I restriction site,
 XX 31 allele, myocardial infarction during percutaneous coronary death,
 XX coronary artery disease, coronary insufficiency, PCR primer, human,
 XX
 XX Homo sapiens.

XX
 XX PN W0200185999-A1;
 XX
 XX PD 15-NOV-2001.
 XX
 XX 10-MAY-2001; 2001WO-US15013.
 XX
 XX 11-MAY-2001; 2000US-204467P.
 XX
 XX (PUB) TUPES COLLEGE.
 XX
 XX Ordway JM, Schaefer EJ;
 XX
 XX WPI; 2002-084904/11.
 XX
 XX Assessing risk for the development of cardiovascular disease in an
 XX individual, comprises analyzing nucleic acid from the individual for
 XX presence of TqII polymorphism of a secretory ring transfer protein
 XX gene -
 XX Claim 13; Page 67; 72pp; English.
 XX
 XX The invention relates to a method for identifying risk for development of
 XX cardiovascular disease, comprising analyzing a nucleic acid from an
 XX individual for the presence of TqII polymorphism of secretory ring
 XX transfer protein (CERP) gene, and assessing the risk for development of
 XX cardiovascular disease. The method involves determining whether the
 XX individual is heterozygous for a polymorphism for a gene for protein
 XX TqII polymorphism, whereby the absence of the polymorphism corresponds
 XX with the frequency and phenotypic expression of coronary artery disease.
 XX The invention also includes PCR primers used for amplification of a
 XX suitable section of the first section of the CERP gene encompassing the
 XX TaqI restriction site of the first allele of the CERP gene. The presence of
 XX the TaqI restriction site being indicative of the absence of the TaqII
 XX polymorphism. The cardiovascular diseases include myocardial infarction,
 XX coronary artery disease, angina pectoris, coronary insufficiency and
 XX coronary death. The sequence represented a PCR primer used in the method
 XX of the invention.
 XX
 XX Sequence 24 BP; 7 A; 7 C; 8 G; 2 T; 0 other;
 XX
 XX Query Match 52.8%; Score 13.2; DB 24; Length 24;
 XX Best local similarity 83.3%; Pred. No. 1e+04;
 XX Matches 15; Conservation 0; Mismatches 3; Indels 0; Gaps 0;
 XX
 XX 5 GCGGCGAAGAAATGACATTC 22
 XX ||||| ||||| |||||
 XX 3 CTACCCGAGAGAGAGAG 20
 XX
 XX RESULT 31
 XX AB197919/C
 XX ID AB197919 standard; DNA; 31 BP.
 XX
 XX AB197919;
 XX
 XX 18 FEB-2002 (first entry)
 XX
 XX Non-endogenous human GRR24 receptor mutagenic primer, SEQ ID NO: 347.
 XX
 XX Human G protein-coupled receptor; GRR24 non endogenous mutant;
 XX constitutively activated GRR24; mutant; human; GRR24;
 XX mutagenic primer; ss.
 XX
 XX Homo sapiens.
 XX
 XX Synthetic.
 XX
 XX W0200177177-A2
 XX
 XX 18-MAY-2001.
 XX
 XX 05-APR-2001; 2001WO-US110998.
 XX
 XX

XX 9 GCCGAGAGATGAGTC 25
 |||||
 DB 18 GCCGAGAGATGAGTC 1

RESULT 27

AA082691/c
 ID AAG27691 (first entry), DNA, 13 bp
 XX

AC AAG26881

XX 14-SEP-1995 (first entry)

XX Cytoskeletal

XX sequence sampled mapping: genome analysis using genome mapping

XX mapped library: 100,000 clones, sequence 100,000 clones, 100,000 clones

XX Cytoskeletal

XX W042488-A

XX 22-DEC-1994

XX 15-JUN-1994 94W0-0506810

XX 15-JUN-1993 93US-0078471

XX 07-SEP-1993 93UC-0117952

XX (SALK) SALK INST BIOLOGICAL STUDIES

XX Evans GA, Smith MW

XX W011 1995-02260206

XX Sequencing: complex genome, present in 100,000 clones

XX then converted with SALK INST BIOLOGICAL STUDIES

XX mammalian chromosomes

XX Example 4: Page 93; 128pp; English

XX Sequences were determined from the ends of chromosome 11-specific

XX cosmids by automated sequencing without intermediate subcloning

XX A sample of 100 DNA fragments from the cosmids were subcloned and

XX these were suitable for the primer identification by PCR

XX analysis (using the "primer" program available from Blander, MIT)

XX The PCR products were mapped by in situ hybridization, and

XX PCR hybrid analysis of both using this method, and PCR specific

XX for human chromosomes 11 were generated and used for PCR

XX regionally mapped. This procedure illustrates a novel method for

XX sequencing complex genomes, designated "sequence sampled mapping"

XX The sequence sampled mapping method is useful for the identification

XX of high density sequence-based maps, and ultimately for the mapping

XX of genomic regions with high density of polymorphisms

XX See AAG2691-94706 and AAG2691-94706 for the primer

XX Sequence 19 bp; 2 A; 6 C; 4 G; 7 T; 0 other

XX Query Match: 52.8%; Score 13.2; DB 15; Length 19;

XX Best local similarity: 92.1%; Pos: 1; Mismatches: 3; Indels: 0;

XX Match: 15; Mismatches: 3; Indels: 0;

XX 4 GCGAGAGATGAGTC 21

XX 19 GCGAGAGATGAGTC 2

XX RESULT 28

XX AAV51660

XX AAV51660 standard; DNA, 21 bp

XX AAV51660

XX 02-FEB-1999 (first entry)

XX Zoa mays genome forward PCR primer #260.

XX Polymorphic marker, allele specific probe, amplification, PCR primer

XX hybridization; plant; hybrid certification; genetic contribution;

XX Pringley, back cross, hybrid, ancestry, corn, ss.

XX Synthetic

XX Zoa mays

XX W0424796-A1

XX 11-JUN-1998

XX 11-SEP-1997 97US-081507

XX 02-DEC-1996; 96US-0032069

XX (APFV-) AFFIRMETRIX INC.

XX Landry EC, Lemieux B, Mulipheux A, Caporale PJ

XX W011 1998-333252/29

XX Example 1: Page 54; 65pp; English

XX AAV51401-VS1704 are forward PCR primers used to amplify fragments of the

XX Zoa mays genome to which the first 100,000 clones were subcloned

XX be used in the construction of allele-specific primers and probes for

XX identification of hybridization (e.g. to determine common or disparate

XX alleles) between a set of fragments from the Zoa mays genome and

XX a set of fragments from the Zoa mays genome and a set of fragments

XX of an ancestral plant, to allow the mapping of polymorphic plants in

XX the construction of a hybrid plant or to identify the history of a

XX back crossed plant with an ancestral plant

XX Sequence 21 bp; 6 A; 8 C; 3 G; 4 T; 0 other

XX Query Match: 52.8%; Score 13.2; DB 15; Length 21;

XX Best local similarity: 92.1%; Pos: 1; Mismatches: 3; Indels: 0;

XX Match: 15; Mismatches: 3; Indels: 0;

XX 1 GCGAGAGATGAGTC 21

XX 19 GCGAGAGATGAGTC 2

XX RESULT 29

XX AAD15821/c

XX AAD15821 standard; DNA, 13 bp

XX AAD15821

XX 15-NOV-2001 (first entry)

XX Homo sapiens

XX W0424796-A1

XX 16-AUG-2001

[illegible][illegible]


```

FT      /tag= h
FT      /mod_base= m5c
FT      18
FT      /tag= i
FT      /mod_base= m5c
FT      20
FT      /tag= j
FT      /mod_base= m5c
FT      20
FT      26 JUL 2001.
FT      W0200152862 At.
FT      12 JAN 2001, 2001W0-0301020.
FT      19-JAN-2001, 20000US-0489765.
FT      (ISIS-) ISIS PHARM INC.
FT      Butler MM, McKay R, Monia BP, Wyatt JB;
FT      WPI; 2001 457510/49.
FT      Novel antisense compounds, particularly oligonucleotides for
FT      inhibiting expression of glycogen synthase kinase 3 beta in cells and
FT      for diagnosing, treating neurological and insulin regulation disorders
FT      .
PS      Claim 3: Page 82, 106pp; English.
XX      CC
XX      CC The invention relates to antisense compounds targeted to
XX      CC nucleic acid encoding glycogen synthase kinase 3 beta (GSK3B)
XX      CC (also known as tau protein kinase 1 (TPK-1)).
XX      CC The antisense compound is useful for inhibiting the expression of
XX      CC glycogen synthase kinase 3 beta enzyme in cells of tissues and for
XX      CC treating diseases or conditions associated with the enzyme
XX      CC such as insulin regulation disorder, in particular diabetes and
XX      CC neurological disorder, e.g. Alzheimer's disease and bipolar
XX      CC illness. The antisense compound is also useful for diagnosing
XX      CC diseases associated with the expression of glycogen synthase kinase
XX      CC 3 beta and for prophylaxis e.g. to prevent or delay infection,
XX      CC inflammation or tumour formation and as a research reagent.
XX      CC The present sequence is an antisense compound targeted to
XX      CC human glycogen synthase kinase 3 beta mRNA.
XX      CC
XX      Sequence ID Ref: 1 At: 7 C: 1 G: 5 T: 0 other.
XX      Query Match 56.0%, Score 14, DB 20, Length 20,
XX      Best Local Similarity 100.0%, Pred. No. 4, e=0.01,
XX      Matches 14, Conservative 0, Mismatch 0, Indels 0, Gaps 0
XX      QY 12 AACAAATGAGGTC 25
XX      16 AAAAAATGAGGTC 3
XX      AAD11520/c
XX      ID AAD11520 standard, RNA, 20 BP.
XX      AC AAD11520;
XX      DT 24 SEP-2001 (first entry)
XX      BE Human glycogen synthase kinase 3 beta antisense oligo HIE 117443.
XX      FM Antisense, glycogen synthase kinase 3 beta, 20BP, diabetes, infection,
XX      FM insulin regulation disorder, neurological disorder, Alzheimer's disease;
XX      FM Fig 1a: 11bp, 11bp, 11bp, 11bp, 11bp, 11bp, 11bp, 11bp, 11bp, 11bp,
XX      FM 10 bp, 10 bp, 10 bp, 10 bp, 10 bp, 10 bp, 10 bp, 10 bp, 10 bp, 10 bp,
XX      OS Homo sapiens.
XX      OS Synthetic.

```

```

XX      XX
XX      Key location/qualifiers
XX      modified_base 1..20
XX      /tag= a
XX      /mod_base= OTHER
XX      /note= "Phosphorothioate backbone"
XX      modified_base 1..5
XX      /tag= b
XX      /mod_base= OTHER
XX      /note= "2' methoxyethyl (2' MOE) nucleotides"
XX      modified_base 16..20
XX      /tag= c
XX      /mod_base= OTHER
XX      /note= "2' methoxyethyl (2' MOE) nucleotides"
XX      modified_base 9
XX      /tag= d
XX      /mod_base= m5c
XX      modified_base 10
XX      /tag= e
XX      /mod_base= m5c
XX      modified_base 12
XX      /tag= f
XX      /mod_base= m5c
XX      modified_base 15
XX      /tag= g
XX      /mod_base= m5c
XX      modified_base 19
XX      /tag= h
XX      /mod_base= m5c
XX      W020157042 At.
XX      26-JUL-2001.
XX      12 JAN 2001, 2001W0-0301020.
XX      19-JAN-2001, 20000US-0489765.
XX      (ISIS-) ISIS PHARM INC.
XX      Butler MM, McKay R, Monia BP, Wyatt JB;
XX      WPI; 2001 457510/49.
XX      Novel antisense compounds, particularly oligonucleotides for
XX      inhibiting expression of glycogen synthase kinase 3 beta in cells and
XX      for diagnosing, treating neurological and insulin regulation disorders
XX      .
PS      Claim 3: Page 82, 106pp; English.
XX      CC
XX      CC The invention relates to antisense compounds targeted to
XX      CC nucleic acid encoding glycogen synthase kinase 3 beta (GSK3B)
XX      CC (also known as tau protein kinase 1 (TPK-1)).
XX      CC The antisense compound is useful for inhibiting the expression of
XX      CC glycogen synthase kinase 3 beta enzyme in cells of tissues and for
XX      CC treating diseases or conditions associated with the enzyme
XX      CC such as insulin regulation disorder, in particular diabetes and
XX      CC neurological disorder, e.g. Alzheimer's disease and bipolar
XX      CC illness. The antisense compound is also useful for diagnosing
XX      CC diseases associated with the expression of glycogen synthase kinase
XX      CC 3 beta and for prophylaxis e.g. to prevent or delay infection,
XX      CC inflammation or tumour formation and as a research reagent.
XX      CC The present sequence is an antisense compound targeted to
XX      CC human glycogen synthase kinase 3 beta mRNA.
XX      CC
XX      Sequence ID Ref: 1 At: 5 C: 1 G: 1 T: 0 other.
XX      Query Match 56.0%, Score 14, DB 20, Length 20,
XX      Best Local Similarity 100.0%, Pred. No. 4, e=0.01,
XX      Matches 14, Conservative 0, Mismatch 0, Indels 0, Gaps 0
XX      QY 12 AACAAATGAGGTC 25

```


C 375	11.4	45.5	25.13	AAV3834	Primer for human 1	C 439	11.2	44.9	24.21	AAZ5522	Mouse anti-human A
C 376	11.4	45.6	29.19	AAV3833	Probe for coding s	C 440	11.2	44.8	24.22	AAZ5523	Cationic emulsifier
C 377	11.4	45.7	29.20	AAV3832	Human HPC9 cDNA ex	C 441	11.2	44.8	24.23	AAZ5524	Human STRAP 2 gene
C 378	11.4	45.6	29.21	AAV3831	Probe used to test	C 442	11.2	44.8	24.24	AAZ5525	Human STRAP 2 gene
C 379	11.4	45.6	29.22	AAV3830	Polymorphic frame	C 443	11.2	44.8	24.25	AAZ5526	Human STRAP 2 gene
C 380	11.4	45.6	29.23	AAV3829	Polymorphic frame	C 444	11.2	44.8	24.26	AAZ5527	Human STRAP 2 gene
C 381	11.4	45.6	29.24	AAV3828	Polymorphic frame	C 445	11.2	44.8	24.27	AAZ5528	Human STRAP 2 gene
C 382	11.4	45.6	29.25	AAV3827	PCR primer beta 1	C 446	11.2	44.8	24.28	AAZ5529	Human STRAP 2 gene
C 383	11.4	45.6	29.26	AAV3826	Human cDNA clone B	C 447	11.2	44.8	24.29	AAZ5530	Human STRAP 2 gene
C 384	11.4	45.6	29.27	AAV3825	Human cDNA clone C	C 448	11.2	44.8	24.30	AAZ5531	Human STRAP 2 gene
C 385	11.4	45.6	29.28	AAV3824	EP retention C bet	C 449	11.2	44.8	24.31	AAZ5532	Human STRAP 2 gene
C 386	11.4	45.6	29.29	AAV3823	Ep retention C bet	C 450	11.2	44.8	24.32	AAZ5533	Human STRAP 2 gene
C 387	11.4	45.6	29.30	AAV3822	Mouse digoxigenin	C 451	11.2	44.8	24.33	AAZ5534	Human STRAP 2 gene
C 388	11.4	45.6	29.31	AAV3821	HSP nucleic acid 1	C 452	11.2	44.8	24.34	AAZ5535	Human STRAP 2 gene
C 389	11.4	45.6	29.32	AAV3820	Strand count star	C 453	11.2	44.8	24.35	AAZ5536	Human STRAP 2 gene
C 390	11.4	45.6	29.33	AAV3819	SV40 antigen nuc	C 454	11.2	44.8	24.36	AAZ5537	Human STRAP 2 gene
C 391	11.4	45.6	29.34	AAV3818	SV40 antigen nuc	C 455	11.2	44.8	24.37	AAZ5538	Human STRAP 2 gene
C 392	11.4	45.6	29.35	AAV3817	SV40 antigen nuc	C 456	11.2	44.8	24.38	AAZ5539	Human STRAP 2 gene
C 393	11.4	45.6	29.36	AAV3816	SV40 antigen nuc	C 457	11.2	44.8	24.39	AAZ5540	Human STRAP 2 gene
C 394	11.4	45.6	29.37	AAV3815	SV40 antigen nuc	C 458	11.2	44.8	24.40	AAZ5541	Human STRAP 2 gene
C 395	11.4	45.6	29.38	AAV3814	SV40 antigen nuc	C 459	11.2	44.8	24.41	AAZ5542	Human STRAP 2 gene
C 396	11.4	45.6	29.39	AAV3813	SV40 antigen nuc	C 460	11.2	44.8	24.42	AAZ5543	Human STRAP 2 gene
C 397	11.4	45.6	29.40	AAV3812	SV40 antigen nuc	C 461	11.2	44.8	24.43	AAZ5544	Human STRAP 2 gene
C 398	11.4	45.6	29.41	AAV3811	SV40 antigen nuc	C 462	11.2	44.8	24.44	AAZ5545	Human STRAP 2 gene
C 399	11.4	45.6	29.42	AAV3810	SV40 antigen nuc	C 463	11.2	44.8	24.45	AAZ5546	Human STRAP 2 gene
C 400	11.4	45.6	29.43	AAV3809	SV40 antigen nuc	C 464	11.2	44.8	24.46	AAZ5547	Human STRAP 2 gene
C 401	11.4	45.6	29.44	AAV3808	SV40 antigen nuc	C 465	11.2	44.8	24.47	AAZ5548	Human STRAP 2 gene
C 402	11.4	45.6	29.45	AAV3807	SV40 antigen nuc	C 466	11.2	44.8	24.48	AAZ5549	Human STRAP 2 gene
C 403	11.4	45.6	29.46	AAV3806	SV40 antigen nuc	C 467	11.2	44.8	24.49	AAZ5550	Human STRAP 2 gene
C 404	11.4	45.6	29.47	AAV3805	SV40 antigen nuc	C 468	11.2	44.8	24.50	AAZ5551	Human STRAP 2 gene
C 405	11.4	45.6	29.48	AAV3804	SV40 antigen nuc	C 469	11.2	44.8	24.51	AAZ5552	Human STRAP 2 gene
C 406	11.4	45.6	29.49	AAV3803	SV40 antigen nuc	C 470	11.2	44.8	24.52	AAZ5553	Human STRAP 2 gene
C 407	11.4	45.6	29.50	AAV3802	SV40 antigen nuc	C 471	11.2	44.8	24.53	AAZ5554	Human STRAP 2 gene
C 408	11.4	45.6	29.51	AAV3801	SV40 antigen nuc	C 472	11.2	44.8	24.54	AAZ555	



JOURNAL Patent: US 5817260 A 01/17/99-1-1-1
 FEATURES
 source Location/Qualifiers
 1..30
 /organism="unknown"
 BASE COUNT 6 a 9 c 9 g 7 t
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 30;
 Best Local Similarity 70.8%; Pred. No. 3.5e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 2 GTCCGAGGCCGAGAAATGAGTC 25
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 CH 7 GTCCGAGGCCGAGAAATGAGTC 30

RESULT 39
 AR075034 AR075034 35 bp DNA linear PAT 28-AUG-2000
 LOCUS
 DEFINITION Sequence 7 from patent US 5855300.
 ACCESSION AR075034
 VERSION AR075034.1 GI:10091786
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 35)
 AUTHORS Faure,F., Herceud,T., Huard,B. and Triebel,F.
 TITLE Soluble polypeptide fragment of the LAG-3 protein, function
 METHOD Therapeutic composition, anti-idiotypic antibodies
 JOURNAL Patent: US 5855300-A / 21-Sep-1999;
 FEATURES
 source Location/Qualifiers
 1..35
 /organism="unknown"

BASE COUNT 10 a 9 c 9 g 7 t
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 35;
 Best Local Similarity 70.8%; Pred. No. 3.5e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 1 CGTCCGAGGCCGAGAAATGAGTC 24
 ||| ||||| ||||| |||||
 CH 7 CGACTTAACCCGAGAACGTGAGGT 30

RESULT 40
 AR118498 AR118498 35 bp DNA linear PAT 16-MAY-2001
 LOCUS
 DEFINITION Sequence 7 from patent US 6143273.
 ACCESSION AR118498
 VERSION AR118498.1 GI:14100391
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 Unclassified.
 REFERENCE 1 (bases 1 to 35)
 AUTHORS Faure,F., Herceud,T., Huard,B. and Triebel,F.
 TITLE Therapeutic composition containing antibodies to soluble
 polypeptide fractions of LAG-3 protein
 JOURNAL Patent: US 6143273 A 7-07-NOV-2000;
 FEATURES
 source Location/Qualifiers
 1..35
 /organism="unknown"

BASE COUNT 10 a 9 c 9 g 7 t
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 35;
 Best Local Similarity 70.8%; Pred. No. 3.5e+05;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 1 GTCCGAGGCCGAGAAATGAGTC 24
 ||| ||||| ||||| |||||

HP /CGATTAAAGGAGAGAGAGAGAGTC 30

Search completed: July 21, 2003, 14:35:16
 CPU time: 00:15:51 secs

REFERENCE 1 (bases 1 to 18)
 AUTHORS Halliwell, P. and Parson, A.
 TITLE Familial Mediterranean fever gene
 JOURNAL Nature
 ORIGIN CREATION 11 (FR); HEIDIG ROLAND (FR)
 FEATURES
 SOURCE /db_xref="taxon:32644"
 /note="polymorphism" 18

BASE COUNT 2 a 4 c 4 g 8 t
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 18;
 Best Local Similarity 87.5%; Pred. No. 3.6e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 4 GAGCCCGGAGAGATCA 21
 |||||
 DB 18 GAGCCCGGAGAGATCA 3

RESULT 31
 AX020014/c
 LOCUS AX020014 21 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 29 from Patient W03037764.
 ACCESSION AX020014
 VERSION AX020014.1 GI:10043943
 KEYWORDS
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Vogelstein, M. P. and David, G. J.
 TITLE New members of the glycogen gene family
 JOURNAL Nature
 ORIGIN CREATION 03 (FR); HEIDIG ROLAND (FR)
 FEATURES
 SOURCE /db_xref="taxon:32644"
 /note="polymorphism" 18

BASE COUNT 2 a 4 c 4 g 8 t
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 19;
 Best Local Similarity 87.5%; Pred. No. 3.6e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 1 GAGCCCGGAGAGATG 20
 |||||
 DB 16 GAGCCCGGAGAGATG 1

BASE COUNT 5 a 5 c 5 g 6 t
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 21;
 Best Local Similarity 87.5%; Pred. No. 3.6e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 6 GAGCCCGGAGAGATGA 21
 |||||
 DB 20 GAGCCCGGAGAGATGA 5

RESULT 32
 AX020070/c
 LOCUS AX020070 21 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 24 from Patient W04037764.
 ACCESSION AX020070
 VERSION AX020070.1 GI:10043900
 KEYWORDS
 SOURCE human
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Vogelstein, M. P. and David, G. J.
 TITLE New members of the glycogen gene family
 JOURNAL Nature
 ORIGIN CREATION 03 (FR); HEIDIG ROLAND (FR)
 FEATURES
 SOURCE /db_xref="taxon:32644"
 /note="polymorphism" 18

BASE COUNT 5 a 5 c 5 g 6 t
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 21;
 Best Local Similarity 87.5%; Pred. No. 3.6e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 6 GAGCCCGGAGAGATGA 21
 |||||
 DB 20 GAGCCCGGAGAGATGA 5

RESULT 33
 AR014507/c
 LOCUS AR014507 24 bp DNA linear PAT 07-SEP-2000
 DEFINITION Sequence 55 from Patient US 5773592.
 ACCESSION AR014507
 VERSION AR014507.1 GI:3371961
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eumetazoa;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Shih, H.-C., Shih, N.-R., Lee, J. and Kang, S.
 TITLE Tumor necrosis factor mutants
 JOURNAL Nature
 ORIGIN CREATION 03 (FR); HEIDIG ROLAND (FR)
 FEATURES
 SOURCE /db_xref="taxon:32644"
 /note="polymorphism" 18

BASE COUNT 2 a 4 c 4 g 8 t
 ORIGIN

Query Match 51.2% Score 12.8; DB 6; Length 20;
 Best Local Similarity 87.5%; Pred. No. 3.6e+05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 10 GAGCCCGGAGAGATG 25
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CY 6 GAGCCGACGAGAGATGAG 23
 11 ||||| ||||| ||
 DB 19 GATCCGACGAGAGATGAG 1

RESULT 21
 LOCUS AX287759/c
 DEFINITION Sequence 145 from Patent WO0179481
 ACCESSION AX287759
 VERSION AX287759.1 GI:17349375
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE Novel methods of constructing libraries of genetic packages that collectively display the members of a diverse family of polypeptides or proteins
 JOURNAL Patent WO 0179481 A 145 (2001-06-06)
 DYNAC CORP. (US)
 FEATURES
 SOURCE
 LOCATION/Qualifiers
 1..22
 /organism="Synthetic construct"
 /db_xref="taxon:10239"
 /note="Synthetic construct"

BASE COUNT 6 a 6 c 4 g 6 t
 ORIGIN

Query Match. Score 13, DB 6, Length 22
 Best Local Similarity 76.2%, Freq. No. 2,964,057
 Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 3 TCCGAGCCGAGAGATGAG 23
 11 ||||| ||||| ||
 DB 21 TCCGAGCCGAGAGATGAG 1

RESULT 22
 LOCUS AX297899/c
 DEFINITION Sequence 285 from Patent WO0179481
 ACCESSION AX297899
 VERSION AX297899.1 GI:17349487
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE Novel methods of constructing libraries of genetic packages that collectively display the members of a diverse family of polypeptides or proteins
 JOURNAL Patent WO 0179481 A 145 (2001-06-06)
 DYNAC CORP. (US)
 FEATURES
 SOURCE
 LOCATION/Qualifiers
 1..22
 /organism="Synthetic construct"
 /db_xref="taxon:10239"
 /note="Synthetic construct"

BASE COUNT 6 a 6 c 4 g 6 t
 ORIGIN

Query Match. Score 13, DB 6, Length 22
 Best Local Similarity 76.2%, Freq. No. 2,964,057
 Matches 16, Conservative 0, Mismatches 0, Indels 0, Gaps 0

RESULT 23
 LOCUS AX012431
 DEFINITION Sequence 32 from Patent EP0955963
 ACCESSION AX012431
 VERSION AX012431.1 GI:3996470
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE Ena sequences encoding enzymes involved in production of isoprenoids
 JOURNAL Patent EP 0955963 A 32 (1999-11-10)
 HOFFMANN LA ROCHE (CH)
 FEATURES
 SOURCE
 LOCATION/Qualifiers
 1..26
 /organism="Synthetic construct"
 /db_xref="taxon:10239"
 /note="primer"

BASE COUNT 12 a 9 c 7 g 2 t
 ORIGIN

Query Match. Score 19, DB 6, Length 26
 Best Local Similarity 76.2%, Freq. No. 2,964,057
 Matches 26, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 1 CTTTCATCTCCGAGAGATGA 21
 11 ||||| ||||| ||
 DB 6 CATGAGAGCCGAGAGAGAGAG 26

RESULT 24
 LOCUS AX116559/c
 DEFINITION Sequence 145 from Patent WO0179481
 ACCESSION AX116559
 VERSION AX116559.1 GI:14033501
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE Novel methods of constructing libraries of genetic packages that collectively display the members of a diverse family of polypeptides or proteins
 JOURNAL Patent WO 0179481 A 145 (2001-06-06)
 DYNAC CORP. (US)
 FEATURES
 SOURCE
 LOCATION/Qualifiers
 1..26
 /organism="Synthetic construct"
 /db_xref="taxon:10239"
 /note="primer"

BASE COUNT 3 a 8 c 2 g 13 t
 ORIGIN

Query Match. Score 13, DB 6, Length 26
 Best Local Similarity 76.2%, Freq. No. 2,964,057
 Matches 13, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 11 CAGAGAGATGAG 23
 11 ||||| ||||| ||
 DB 13 CAGAGAGATGAG 1

RESULT 25
 LOCUS ES1024
 DEFINITION Improved production of isoprenoid
 ACCESSION ES1024
 VERSION ES1024.1 GI:13023246
 KEYWORDS
 SOURCE
 LOCATION/Qualifiers
 1..26
 /organism="Synthetic construct"
 /db_xref="taxon:10239"
 /note="primer"

BASE COUNT 26 bp
 ORIGIN

Query Match. Score 13, DB 6, Length 26
 Best Local Similarity 76.2%, Freq. No. 2,964,057
 Matches 13, Conservative 0, Mismatches 0, Indels 0, Gaps 0

JOURNAL Patent: US 560886-A 6 04 MAY 1997
 LOCATION/Qualifiers
 SOURCE 1.30
 /organism="unknown"
 BASE COUNT 10 a 7 c 7 g 6 t
 ORIGIN

Query Match 53.6% Score 13.4; DP 6; Length 30;
 Best Local Similarity 53.6%; Fred No. 1.9e+05;
 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528
 DEFINITION Sequence 6 from patent US 560886-A
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

RESULT 12
 LOCUS AR067333
 DEFINITION Sequence 8 from patent US 560886-A
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

REFERENCE 1 (bases 1 to 30)
 AUTHORS Cho, S., Jeremy, A. and Strominger, J. L.
 TITLE Transcription factor regulating hmg expression cDNA and genomic
 clones encoding same and their utility in identifying hmg
 Patent: US 560886-A 6 04 MAY 1997
 LOCATION/Qualifiers
 SOURCE 1.30
 /organism="unknown"

BASE COUNT 10 a 7 c 7 g 6 t
 ORIGIN

Query Match 53.6% Score 13.4; DP 6; Length 30;
 Best Local Similarity 53.6%; Fred No. 1.9e+05;
 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528
 DEFINITION Sequence 6 from patent US 560886-A
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

RESULT 13
 LOCUS 136528
 DEFINITION Sequence 6 from patent US 560886-A
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

REFERENCE 1 (bases 1 to 30)
 AUTHORS Boucher, R. C., Weisman, G. A., Turner, J. T., Harden, T. K., Parry, G. E.,
 Sullivan, D. M., Erb, L. J. and Lustig, K. D.
 TITLE DNA Encoding the human P subunit receptor and full length -q-receptor
 P subunit receptors
 Patent: US 560886-A 6 04 MAY 1997
 LOCATION/Qualifiers
 SOURCE 1.30
 /organism="unknown"

BASE COUNT 8 a 4 c 12 g 1 t 5 others
 ORIGIN

Query Match 53.6% Score 13.4; DP 6; Length 30;
 Best Local Similarity 53.6%; Fred No. 1.9e+05;
 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528
 DEFINITION Sequence 6 from patent US 560886-A
 ACCESSION AR067333
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 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

RESULT 14
 LOCUS 136528
 DEFINITION Sequence 6 from patent US 560886-A
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

REFERENCE 1 (bases 1 to 30)
 AUTHORS Boucher, R. C., Weisman, G. A., Turner, J. T., Harden, T. K., Parry, G. E.,
 Sullivan, D. M., Erb, L. J. and Lustig, K. D.
 TITLE DNA Encoding the human P subunit receptor and full length -q-receptor
 P subunit receptors
 Patent: US 560886-A 6 04 MAY 1997
 LOCATION/Qualifiers
 SOURCE 1.30
 /organism="unknown"

BASE COUNT 8 a 4 c 12 g 1 t 5 others
 ORIGIN

Query Match 53.6% Score 13.4; DP 6; Length 30;
 Best Local Similarity 53.6%; Fred No. 1.9e+05;
 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528
 DEFINITION Sequence 6 from patent US 560886-A
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
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 SOURCE 1.30
 /organism="unknown"

RESULT 15
 LOCUS 136528
 DEFINITION Sequence 6 from patent US 560886-A
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

REFERENCE 1 (bases 1 to 30)
 AUTHORS Boucher, R. C., Weisman, G. A., Turner, J. T., Harden, T. K., Parry, G. E.,
 Sullivan, D. M., Erb, L. J. and Lustig, K. D.
 TITLE Method of inhibiting cell growth with the P subunit receptor
 Patent: US 560886-A 6 04 MAY 1997
 LOCATION/Qualifiers
 SOURCE 1.30
 /organism="unknown"

BASE COUNT 8 a 4 c 12 g 1 t 5 others
 ORIGIN

Query Match 53.6% Score 13.4; DP 6; Length 30;
 Best Local Similarity 53.6%; Fred No. 1.9e+05;
 Matches 14, Conservative 5, Mismatches 6, Indels 0, Gaps 0

LOCUS 136528
 DEFINITION Sequence 6 from patent US 560886-A
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

RESULT 16
 LOCUS AR067333
 DEFINITION Sequence 601 from patent US 5651760.
 ACCESSION AR067333
 VERSION 1.0
 KEYWORDS
 ORGANISM Unknown.
 SOURCE 1.30
 /organism="unknown"

LOCUS AX119621 22 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 24 from Patent WO0129213.
 ACCESSION AX119621
 VERSION AX119621.1 GI:14016529
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 BASE COUNT 7 a 3 c 8 g 4 t
 ORIGIN
 Query Match 54.4% Score 13.6 DB 6 Length 22;
 Best Local Similarity 80.0% Pred. No. 1.5e+05;
 Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0;
 Oy 5 GCGAGGAAATACATACAT 24
 1 ||| ||| ||| ||| |||
 2 CAACTCAGAAAGATGATGAT 21
 3
 RESULT 8
 LOCUS AX107613 20 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 132 from Patent WO0133652.
 ACCESSION AX107613
 VERSION AX107613.1 GI:1442992
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 BASE COUNT 12 a 4 c 9 g 5 t
 ORIGIN
 Query Match 54.4% Score 13.6 DB 6 Length 30;
 Best Local Similarity 80.0% Pred. No. 1.5e+05;
 Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0;
 Oy 2 GCGAGGAAATACATACAT 24
 1 ||| ||| ||| ||| |||
 6 GTAAGATCCTGAAAGATGTA 25
 7
 RESULT 9
 LOCUS AX107624 30 bp DNA linear PAT 30-APR-2001
 DEFINITION Sequence 343 from Patent WO0133652.
 ACCESSION AX107624
 VERSION AX107624.1 GI:1442999
 KEYWORDS

SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 BASE COUNT 12 a 4 c 9 g 5 t
 ORIGIN
 Query Match 54.4% Score 13.6 DB 6 Length 30;
 Best Local Similarity 80.0% Pred. No. 1.5e+05;
 Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0;
 Oy 2 GCGAGGAAATACATACAT 21
 1 ||| ||| ||| ||| |||
 6 GTAAGATCCTGAAAGATGTA 25
 7
 RESULT 10
 LOCUS AX116224 27 bp DNA linear PAT 11-MAY-2001
 DEFINITION Sequence 114 from Patent WO0129213.
 ACCESSION AX116224
 VERSION AX116224.1 GI:14016516
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 SOURCE
 BASE COUNT 9 a 3 c 14 g 1 t
 ORIGIN
 Query Match 54.4% Score 13.4 DB 6 Length 27;
 Best Local Similarity 87.0% Pred. No. 1.3e+05;
 Matches 14, Conservative 0, Mismatches 2, Indels 0, Gaps 0;
 Oy 8 GCGAGGAAATACATACAT 23
 1 ||| ||| ||| ||| |||
 2 GACCAAGATGATGATGAT 17
 3
 RESULT 11
 LOCUS AR060636 29 bp DNA linear PAT 29-SEP-2000
 DEFINITION Sequence 8 from patent US 5448412.
 ACCESSION AR060636
 VERSION AR060636.1 GI:5967096
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE

```

FEATURES
SOURCE
Variation
5'UTR
Variation
CDS
BASE COUNT
ORIGIN
CY
DB
17
RESULT 7
AX119631

```


[illegible]

REFERENCE

AUTHORS

1 (bases 1 to 23)
 Altschul, S. M., Levenson, T. J., Rajas, P., Chen, H., Cheuk, P., Gadinab,
 C., Jeske, A., Karnes, M., Kim, C. J., Parvizi, H., Pridits, L., Shinn, P.,
 Zimmerman, J., and Ecker, J. R.

TITLE

A Sequence-Indexed Library of Insertion Mutations in the
 Arabidopsis Genome

JOURNAL

Unpublished (2001)

COMMENT

Contact: Joseph R. Ecker
 Salk Institute Genomic Analysis Laboratory (SIGAL)
 The Salk Institute for Biological Studies
 10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
 Tel: 858 453 4100 x1752
 Fax: 858 558 6379
 Email: ecker@salk.edu

This is single first sequence retrieved from the left border of
 TDNA.

FEATURES

Source

Class: TDNA tagged.

Location/Qualifiers

1..23
 /organism="Arabidopsis thaliana"
 /strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_063270.52.90.x"

/clone_lib "Arabidopsis thaliana TDNA insertion lines"

/notes="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://salk.edu/tdna_protocols.html"

BASE COUNT

17 a 2 c 2 g 2 t

ORIGIN

Query Match

40.7% Score 11; Dp 17; Length 23;

Fast Local Similarity

73.7% Pred. No. 2e+06; 5; Indels 0; Gaps 0;

Matches

14; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY

9 AATACCTAACGACCAATA 27

DB

3 AATAACTTACGACCAATA 21

Search completed: July 21, 2003, 15:47:50
 Job time : 713.784 secs

TITLE
Islam H., Longacre, S., Mahmood, M., Meenen, E., Pedersen, T., Reilly
M., Rice, W., Sorensen, J., van der, T., Wang, F., Wang, A., van, M.,
and Wright, D., Weiss, R.
Mouse whole genome scaffolding with paired end reads from 10kb

Islam, H., Donachie, S., Mahmoud, M., Morgan, E., Pridmore, C., Pott, J. M., Farnham, R. G., P. de Vos, P., Gregory, A., and Nicholson, P. K. and Wright, D., Weiss, P. Muscle whole-genome scaffolding with paired-end reads from 10th

FEATURES

- Local Job/Candidate

Localities/Qualifiers

[illegible]

	C	GAACTACTAGGACA	23
	6	CAAAACCAACAACA	21
DB			
RESULT 38			
A2346787			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
ATTACHES			

BASE COUNT 6 a 8 c 7 g 13 t
 ORIGIN
 Query Match 43.0%; Score 11.6; DB 17; Length 34;
 Best Local Similarity 77.8%; Pred. No. 1.2e+06;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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 31 TGAAGACCACTAAGAA 14

RESULT 24
 A2431916 45 bp DNA linear GSS 14 DEC 2000
 LOCUS
 DEFINITION 1M0217C71F Mouse 10kb plasmid U05GCM library Mus musculus genomic
 clone U05GCM10217C71 F, DNA sequence
 ACCESSION A2431916 GI:10556025
 VERSION A2431916.1 GI:10556025
 KEYWORDS
 SOURCE GSS
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 35)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvai, R., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rolly,
 M., Rose, M., Rose, R., Stokes, P., Tinney, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 26 S. 2020 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0217 row: C column: 21
 Seq primer: CCGTGTAAACGACGCTTACT
 Class: plasmid ends
 High quality sequence stop: 35.
 Location/Qualifiers
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 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U05GCM10217C21"
 /clone_lib="Mouse 10kb plasmid U05GCM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /note="Vector: pMD229; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/headers/). The DNA
 was hydrolytically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adapter oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapter DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (91473114/95/AF129072.1), a copy number
 inducible derivative of plasmid R1. The vector was ligated
 with adapters complementary to the insert adapters and
 purified. The sheared, adapter mouse DNA was annealed to
 adapter vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

BASE COUNT 3 a 6 c 8 g 18 t
 ORIGIN
 Query Match 43.0%; Score 11.6; DB 17; Length 34;
 Best Local Similarity 77.8%; Pred. No. 1.2e+06;
 Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

9 TATACCTAACGACCAAT 26
 |||||
 34 AAAAATATATACACAT 17

RESULT 25
 A2581676 24 bp DNA linear GSS 14 DEC 2000
 LOCUS
 DEFINITION 1M0217C71F Mouse 10kb plasmid U05GCM library Mus musculus genomic
 clone U05GCM10217C71 F, DNA sequence
 ACCESSION A2581676 GI:11630526
 VERSION A2581676.1 GI:11630526
 KEYWORDS
 SOURCE GSS
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;
 1 (bases 1 to 24)
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duvai, R., Hamill, C.,
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rolly,
 M., Rose, M., Rose, R., Stokes, P., Tinney, A., von Niederhausern, A.,
 and Wright, D., Weiss, R.
 Mouse whole genome scaffolding with paired end reads from 10kb
 plasmid inserts
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Robert B. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 26 S. 2020 E., SLC, UT
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0217 row: N column: 06
 Seq primer: CACACGGAACGACGCTTACT
 Class: plasmid ends
 High quality sequence stop: 24.
 Location/Qualifiers
 1..24
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U05GCM10217C06"
 /clone_lib="Mouse 10kb plasmid U05GCM library"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Ti-resistant, F-"
 /note="Vector: pMD229; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/headers/). The DNA
 was hydrolytically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adapter oligonucleotides were
 ligated to the blunt ends in high molar excess. The
 adapter DNA was purified and size-selected for a 9.5 to
 10.5 kb range using preparative agarose gel
 electrophoresis. Vector DNA was prepared from a derivative
 of pMD22 (91473114/95/AF129072.1), a copy number
 inducible derivative of plasmid R1. The vector was ligated
 with adapters complementary to the insert adapters and
 purified. The sheared, adapter mouse DNA was annealed to
 adapter vector DNA, and transformed into
 chemically-competent E. coli XL10-Gold (Stratagene) cells
 and selected for ampicillin resistance."

Fax: 858 558 6179
Email: eckersalk.edu

This is single pass sequence recovered from the left border of
TMA.

Class: TMA tagged

FEATURES
SOURCE

1..29

/organism="Arabidopsis thaliana"
/strain="Columbia 0"

/db_xref="taxon:1073"

/clone="SAIK_059112.40.40.X"

Notes: The Arabidopsis thaliana TMA insertion lines
insertion was performed on Arabidopsis thaliana lines
each of which contains one or more TMA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the position of the
site of insertion. Details of the protocols used can
be found at <http://www.salk.edu/maibach/>

BASE COUNT 13 a 4 c 3 g
ORIGIN

Query Match 43.0% Score 11.6 DB 17 Length 29

Best Local Similarity 77.9% Prob 0.000000

Match 10 Constructive 0 Mismatches 4 Indels 0 Gaps 0

4 TACGATCTTACGAT 21
||||| |||||
3 TACGATCTTACGAT 20

DB

RESULT 22

LOCUS

DEFINITION SALK_059112.40.40.X TMA insertion line Arabidopsis

ACCESSION BH663155

VERSION BH663155

KEYWORDS

ORGANISM

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BASE COUNT 13 a 3 c 2 g 11 t
ORIGIN

Query Match 43.0% Score 11.6 DB 17 Length 29

Best Local Similarity 77.9% Prob 0.000000

Match 10 Constructive 0 Mismatches 4 Indels 0 Gaps 0

4 TACGATCTTACGAT 26
||||| |||||
12 TACGATCTTACGAT 23

DB

Notes: The Arabidopsis thaliana TMA insertion lines
insertion was performed on Arabidopsis thaliana lines
each of which contains one or more TMA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the position of the
site of insertion. Details of the protocols used can
be found at <http://www.salk.edu/maibach/>

BASE COUNT 13 a 3 c 2 g 11 t
ORIGIN

Query Match 43.0% Score 11.6 DB 17 Length 29

Best Local Similarity 77.9% Prob 0.000000

Match 10 Constructive 0 Mismatches 4 Indels 0 Gaps 0

4 TACGATCTTACGAT 26
||||| |||||
12 TACGATCTTACGAT 23

DB

RESULT 23

LOCUS

DEFINITION SALK_059112.40.40.X TMA insertion line Arabidopsis

ACCESSION BH663155

VERSION BH663155

KEYWORDS

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PAGE COUNT
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2x 2 CCGAGCAATATCTTAACGACCA 24
||| ||| ||| ||| |||
Dn 1 CCTAGCCCTACACAAACACCA 23

RESULT	3
EMERGENCY	0809496/c
LOCUS	BH953496
DEFINITION	CAMP-07000-40 OF 2 PARTS: 1st PART CONTAINS 1ST AND 2ND

ACCESSION	BRH53496
VERSION	BRH53496.1
KEYWORDS	CD44 CD44P1
SYNOPSIS	CD44 CD44S
ORIGINATOR	CD44 CD44S
DESCRIPTION	CD44 CD44S

RECEIVED	DATE	FROM	TO
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TITLE: *Seigneurie inférieure: l'histoire de l'histoire* W. G. Sebald
 JOURNAL: *Arthropos* (Germany)
 PUBLISHED: (2001)
 COMMENT: Contact: *arpos@f.fh-erlangen.de*

This is a single pass sequencing protocol from the 100 kb library of cDNA. This sequence has been deposited in the EMBL database under accession number AF592060. Class: rRNA tagged.

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      /note="The Arabidopsis thaliana TMM insertion lines"
      /note="PCR was performed on Arabidopsis thaliana lines"
      each of which contains one or more TMM insertion
      elements. The resultant fragment for each line was

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Country	Year	Age	Sex	Length	Wing	Tail	Culmen	Weight
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United States	1964	80-89	Female	227	117	100	15	10.5
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United States	1964	110-119	Female	227	117	100	15	10.5
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United States	1964	410-419	Female	227	117	100	15	10.5
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08 11 AACTTAACTAACCAATA 1
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09 12 AACTTAACTAACCAATA 1

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RESULT 4
2569185

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Accession	U00001
Version	1
Release Date	1980-01-01
Update Date	2005-11-01
Accession	U00001
Version	1
Release Date	1980-01-01
Update Date	2005-11-01

SOURCE	human.
ORGANISM	<i>Homo sapiens</i>
EXTRACT	Embryoid, Neural, Glial, Neural, Neural, Vertebrate, Vertebrate

REFERENCE	AUTHORS	TITLE
1 (pages 1 to 35)	NIH-MG7 http://mgc.ncbi.nlm.nih.gov/ .	National Institutes of Health, Mammalian Gene Collection. MG7

CONTACT: Robert Strausberg, Ph.D.
Email: cgabbs-femail.nih.gov
Tissue Procurement: CLOUTCH Laboratories, Inc.

[illegible]

FEATURES	POSITION/QUALITERS
source	1, 35

[illegible]

Query Match	48.8%	Score 13.27	EB 12	Length 35
Best local similarity	59.2% <td>Prod. No. 2, 4/05</td> <td></td> <td></td>	Prod. No. 2, 4/05		
Matches 16	Conservation 0	Mismatches 0		

[illegible]

REPORT
ON
TATSAO/C

[illegible]

ALIGNMENTS

[illegible]

RESULT 1	
PM813368	
LOCUS	PM813368
DEFINITION	Partial Arabidopsis thaliana DNA insert, lines Arabidopsis
ACCESSION	thaliana genome clone SAIR_064724, DNA sequence
VERSION	PM813368
KEYWORDS	Arabidopsis thaliana
SOURCE	GenBank
ORGANISM	thale cress, Arabidopsis thaliana Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Euphyllophytes, Angiosperms, Rosales, Brassicaceae, Brassicaceae, Brassicaceae Arabidopsis 1 (bases 1 to 35)
REFERENCE	
AUTHORS	Alonso, J.M., Leister, T.J., Barajas, F., Chen, H., Cheek, F., Gadgil J., Jocke, A., Karsenti, M., Kim, J., Parker, H., Pridmore, A., Shinozaki, K., Zimmermann, J., and Ecker, J.R.
TITLE	A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
JOURNAL	Unpublished (2001)
COMMENT	Contact: Joseph R. Ecker Salk Institute for Biological Studies The Salk Institute for Biological Studies

JOURNAL
COMMENT

plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Center
for Human Genome Research
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 76 S. 1400 E., Salt Lake City,
UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: dunn@genetics.utah.edu
Insert length: 10000 bp; EPRC: 0.09
Plasmid size: 11.0 kb; plasmid ID: 124
Seq primer: CTGTTTAAATTAAGTCTTCACCAT
Class: plasmid ends
High quality sequence stop: 32
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[illegible]

[illegible]

[illegible]

[illegible]

RESULT 32
US-10-269-557-88
Sequence 4: Artificially Generated
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: University of Illinois
TITLE OF INVENTION: Therapeutic Agent
FILE REFERENCE: UNIPATSPOT
CURRENT AFFILIATION NUMBER: 001-11-13
CURRENT FILING DATE: 2001-04-12
PRIORITY FILING DATE: 1998-04-09
PRIORITY FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 19
TYPE: DNA
ORGANISM: Homo sapiens
US-10-269-557-88

Query Match 47.4% Score 12.8; DB 15; Length 19;
Best Local Similarity 87.0; Field No. 246+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 CTGAGCAATACCTAAC 18
DB 16 CTGAGCAATACCTAAC 1

RESULT 33
US-10-269-557-89/0
Sequence 88: Application US/10269557
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Micromedex, Inc.
TITLE OF INVENTION: HEPATOCYTE GENE AND PROMOTER FROM
TITLE OF INVENTION: HEPATOCYTE GENE AND PROMOTER FROM
FILE REFERENCE: 870103.411
CURRENT AFFILIATION NUMBER: 001-11-13
CURRENT FILING DATE: 2001-04-12
PRIORITY FILING DATE: 1998-04-09
PRIORITY FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 88
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HEPATOCYTE GENE AND PROMOTER FROM
OTHER INFORMATION: Gene and its promoter Artificially Generated (Hepo)
OTHER INFORMATION: expression plasmids
US-10-269-557-88

Query Match 47.4% Score 12.8; DB 15; Length 19;
Best Local Similarity 87.0; Field No. 246+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 CTGAGCAATACCTAAC 18
DB 16 CTGAGCAATACCTAAC 1

RESULT 34
US-10-269-557-89/0
Sequence 41: Artificially Generated
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: MICROMEDEX, INC.
TITLE OF INVENTION: HEPATOCYTE GENE AND PROMOTER FROM
FILE REFERENCE: 870103.411
CURRENT AFFILIATION NUMBER: 001-11-13
CURRENT FILING DATE: 2001-04-12
PRIORITY FILING DATE: 1998-04-09
PRIORITY FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HEPATOCYTE GENE AND PROMOTER FROM
OTHER INFORMATION: Gene and its promoter Artificially Generated (Hepo)
OTHER INFORMATION: expression plasmids
US-10-269-557-88

CURRENT AFFILIATION NUMBER: 001-11-13
CURRENT FILING DATE: 2001-04-12
PRIORITY FILING DATE: 1998-04-09
PRIORITY FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 41
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificially Generated (Hepo)
US-10-118-079-41

Query Match 47.4% Score 12.8; DB 15; Length 19;
Best Local Similarity 87.0; Field No. 246+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 CTGAGCAATACCTAAC 18
DB 16 CTGAGCAATACCTAAC 1

RESULT 35
US-10-098-2538-26931
Sequence 26931: Application US/100982638
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT AFFILIATION NUMBER: 001-11-13
CURRENT FILING DATE: 2001-04-12
PRIORITY FILING DATE: 1998-04-09
PRIORITY FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26931
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2538-26931

Query Match 47.4% Score 12.8; DB 15; Length 25;
Best Local Similarity 70.8; Field No. 246+04;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

1 CTGAGCAATACCTAAC 24
DB 1 CTGAGCAATACCTAAC 24

RESULT 36
US-10-098-2538-26931
Sequence 26931: Application US/100982638
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT AFFILIATION NUMBER: 001-11-13
CURRENT FILING DATE: 2001-04-12
PRIORITY FILING DATE: 1998-04-09
PRIORITY FILING DATE: 1998-04-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn version 3.1
SEQ ID NO 26931
LENGTH: 25
TYPE: DNA

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Primer
 US 09-771-943-141

Query Match 48.1% Score 12.8; DB 1% Length 19
 Best Local Similarity 87.5% Pred. No. 2.4e+04
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 5 GAGCAATACCTAACCAAA 25
 DB 21 GAGCAATATTTACAAACAA 1

RESULT 28
 US 09-812-777-8/c

Sequence 9, Application US/0981277
 Publication No. US20020115827A1
 GENERAL INFORMATION:
 APPLICANT: KIM, KEY SUN
 TITLE OF INVENTION: A METHOD FOR DNA SEQUENCING
 FILE REFERENCE: US/09-812-777
 CURRENT APPLICATION NUMBER: US/09-812-777
 CURRENT FILING DATE: 2001-04-14
 PRIOR APPLICATION NUMBER: US 09-63506
 PRIOR FILING DATE: 2000-10-27
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: Patent in Ver. 2.1
 SEQ ID NO 8
 LENGTH: 19
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Primer
 US 09-812-777-8

Query Match 47.4% Score 12.8; DB 1% Length 19
 Best Local Similarity 87.5% Pred. No. 2.4e+04
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 3 CTGAGCAATACCTAAC 18
 DB 16 CTGAGCAATACCTAGC 1

RESULT 29
 US 09-947-172-16/c

Sequence 36, Application US/0994712
 Publication No. US20010007079A1
 GENERAL INFORMATION:
 APPLICANT: CENTER FOR HEALTH AND SCIENCE UNIVERSITY
 APPLICANT: VANSEBARY, ARTHUR A
 TITLE OF INVENTION: FEEDBACK METHOD FOR DETECTING THE EFFECT OF MANIPULATION OF AIL-1 GEN-360
 FILE REFERENCE: US/09-58137
 CURRENT APPLICATION NUMBER: US/09-947-172
 CURRENT FILING DATE: 2001-07-01
 PRIOR APPLICATION NUMBER: US 09-500,342
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: US 09/153,586
 PRIOR FILING DATE: 1998-09-16
 PRIOR APPLICATION NUMBER: US 09/064,555
 PRIOR FILING DATE: 1997-10-10
 PRIOR APPLICATION NUMBER: US 09/064,502
 PRIOR FILING DATE: 1997-09-16
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: Patent in Version 3.1
 SEQ ID NO 46
 LENGTH: 19
 TYPE: DNA
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: PCR primer
 US 09-947-172-36

Query Match 47.4% Score 12.8; DB 1% Length 19
 Best Local Similarity 87.5% Pred. No. 2.4e+04
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 3 CTGAGCAATACCTAAC 18
 DB 16 CTGAGCAATACCTAGC 1

RESULT 30
 US-10-260-351-4/c

Sequence 4, Application US/10260351
 Publication No. US20010006753A1
 GENERAL INFORMATION:
 APPLICANT: University of Bristol
 TITLE OF INVENTION: Therapeutic Agent
 FILE REFERENCE: US/09-150,150
 CURRENT APPLICATION NUMBER: US/10-260-351
 CURRENT FILING DATE: 2001-10-01
 PRIOR APPLICATION NUMBER: US/09-077,921
 PRIOR FILING DATE: 1998-04-09
 NUMBER OF SEQ ID NOS: 16
 SOFTWARE: Patent in Version 3.1
 SEQ ID NO 4
 LENGTH: 19
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-260-351-4

Query Match 47.4% Score 12.8; DB 1% Length 19
 Best Local Similarity 87.5% Pred. No. 2.4e+04
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 3 CTGAGCAATACCTAAC 18
 DB 16 CTGAGCAATACCTAGC 1

RESULT 31
 US-10-216-705-7/c

Sequence 7, Application US/10216705
 Publication No. US20030096973A1
 GENERAL INFORMATION:
 APPLICANT: Meristem Therapeutics, S.A.
 TITLE OF INVENTION: Methods for detecting and identifying proteins produced by bacteria, Mycobacterium tuberculosis, and other organisms
 FILE REFERENCE: US/09-331,347
 CURRENT APPLICATION NUMBER: US/10-216-705
 CURRENT FILING DATE: 2002-08-09
 PRIOR APPLICATION NUMBER: US 09/331,347
 PRIOR FILING DATE: 1999-08-17
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: Patent in Version 3.1
 SEQ ID NO 7
 LENGTH: 19
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: T7 promoter primer
 US-10-216-705-7

Query Match 47.4% Score 12.8; DB 1% Length 19
 Best Local Similarity 87.5% Pred. No. 2.4e+04
 Matches 14; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 3 CTGAGCAATACCTAAC 18
 DB 16 CTGAGCAATACCTAGC 1

Query Match 48.1% Score 13 DB 15 Length 25
Best Local Similarity 76.0% Filed No. 2004-05-10-13
Matches 16 Conserved 0 Mismatches 5 Indels 0

CY 5 GAGCAATACCTTACGACACCA 25
DB 22 GTCCAGTACCTTACGACACCA 2

RESULT 23

US-10-098-263B-78252

Sequence 2383, Application US/098-263B
Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human MHC Class II

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-02-08

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 13066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 23739

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-098-263B-78252

Query Match 48.1% Score 13 DB 15 Length 25
Best Local Similarity 76.0% Filed No. 2004-05-10-13
Matches 16 Conserved 0 Mismatches 5 Indels 0

CY 5 GAGCAATACCTTACGACACCA 25
DB 25 GAGCAATACCTTACGACACCA 5

RESULT 24

US-10-098-263B-78252

Sequence 7622, Application US/098-263B
Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-02-08

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 13066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 7622

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-098-263B-78252

Query Match 48.1% Score 13 DB 15 Length 25
Best Local Similarity 76.0% Filed No. 2004-05-10-13
Matches 16 Conserved 0 Mismatches 5 Indels 0

CY 1 TCTGTGATGATGATGATGAT 21
DB 4 TCTGTGATGATGATGATGAT 24

RESULT 25

US-10-098-263B-78252

Sequence 12451, Application US/098-263B
Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-02-08

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 13066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 12451

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/10/098-263B

CURRENT FILING DATE: 2003-01-08

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 13066

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO 12451

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-098-263B-78252

Query Match 48.1% Score 13 DB 15 Length 25
Best Local Similarity 76.0% Filed No. 2004-05-10-13
Matches 16 Conserved 0 Mismatches 5 Indels 0

CY 5 GAGCAATACCTTACGACACCA 25
DB 24 GTCCAGTACCTTACGACACCA 4

RESULT 26

US-09-864-636A-2383

Sequence 2383, Application US/098-636A
Publication No. US20030104376A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/09/864-636A

CURRENT FILING DATE: 2002-10-15

NUMBER OF SEQ ID NOS: 2640

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2383

LENGTH: 28

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic

US-09-864-636A-2383

Query Match 48.1% Score 13 DB 12 Length 28
Best Local Similarity 76.0% Filed No. 2004-05-10-13
Matches 16 Conserved 0 Mismatches 5 Indels 0

CY 3 GAGCAATACCTTACGACACCA 23
DB 6 CTGAGCAATACCTTACGACACCA 28

RESULT 27

US-09-771-933-141C

Sequence 141, Application US/097-933
Publication No. US2003010387A1

GENERAL INFORMATION:

APPLICANT: Mittman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 620-130

CURRENT APPLICATION NUMBER: US/09/771-933

CURRENT FILING DATE: 2001-01-30

NUMBER OF SEQ ID NOS: 205

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 141

LENGTH: 30

TYPE: DNA

ORGANISM: Homo sapiens

US-09-771-933-141C

RESULT 18
 US-10-153-902-9
 Sequence 9, Affiliation: US/1013392
 File ID: 1013392
 GENERAL INFORMATION
 APPLICANT: STEIN, EDWARD
 TITLE OR INVENTION: VACUINE DELIVERY SYSTEM
 FILE REFERENCE: 2747-0097-27 CIP (R014-014)
 CURRENT APPLICANT NUMBER: 02/10/153/722
 CURRENT FILING DATE: 2002-05-24
 PRIOR APPLICATION NUMBER: 05/07/081,576
 PRIOR FILING DATE: 1998-05-19
 PRICE AFFILIATION NUMBER: 02/10/153/722
 PRIOR FILING DATE: 1997-09-23
 PRIOR APPLICATION NUMBER: US 08/443,514
 PRIOR FILING DATE: 1995-05-19
 NUMBER OF CIP ID NOS.: 1
 SOFTWARE: Patent In Vent. 2 0
 SEQ ID NO 9
 LENGTH: 15
 TYPE: DNA
 CRYMIL-2X, Nucleotide sequence
 US-10-153-902-9

Query Match	48.9%	Score 13.2	DB 15	Length 35
Best Local Similarity	48.8%	Prod No 17a04		
Matches	142	Matched bases	10	Indels 2

2y	9	AATACCTAACGAACAAT	26
fb	12	AAATCTAATCAACAAAT	29

RESULT 19
US 09-764-R52A-Q197-

1 Sequence: 819, Affected: 106, 152, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980,

Query Match	49.1%	Score 13	EP 12	Length 25
Pos. Count	76.0%	Prod. MC	2e.0%	
Matches	16	of Mis-matches	5	Indices
				Days

0Y	3	CTTACGATATACCTTACCGACCA	2
1b	25	CTTACGATATACCTTACCGACCA	5

RESULT 20
05-10-214 112 1417/0

; Publication No. US2003008251
; GENERAL INFORMATION;
; APPLICANT: Michael Muttman

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Query Match:	49.18;	Score 13;	DR 15;	Length 20;
Best Local Similarity:	70.43;	Field No. 4474;		
Matches 16;	Conservative 0;	Mismatches 5;	Indels 1;	gaps 7

4 TGAGCATACCTTAACGACAA 24
|||||
25 TGAAGTAAGCTTAAGCAATA 5

RESULT 21
US-10-098

Publication No. HS20030104410A1
GENERAL INFORMATION

```

: GENERAL INFORMATION:
: APPLICANT: Miltman, Michael
: TITLE OF INVENTION: Human Microarray
: FILE REFERENCE: 318.1
: CURRENT APPLICATOR NUMBER: 06/10/000 303B

```

1 CURRENT APPLICATION NUMBER: 06/407,928, 263 B
2
3 CURRENT FILING DATE: 2003-01-08
4
5 PRICE APPLICATION: 567,276,759
6
7 PRICE FILING DATE: 2001-03-16
8
9 AMENDED STATEMENT: 120006

```

1  NUMBER OF SEQ ID NOS: 131095
2
3  SEQUENCE: Multiple alignment from sequence listing for entry V 1
4  SEQ ID NO 16473
5
6  LENGTH: 25
7
8  TYPE: DNA

```

TYPE: DNA
ORGANISM: Homo sapiens
MS-10-098-263B-16473

Query Match	48.18%	Score 137	DB 1st	Genbank
East Lake, Sitka, Alaska	99.8%	136.9	100.4%	0.000000
Marches 1st, Representative	0%			0.000000
				0.000000

```

cy      5  GAGCAATACCTTAACTGAAAGAA 28
          |||||
Db      21  GTGCACCTACCTAACCTAGTAA 1

```

RESULT 22
MS-10-000

Publication No. US20030104410A1
GENERAL INFORMATION

GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: HUMAN MOTONEROY
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: 16,710,000 (23)

1 CURRENT APPLICATION NUMBER: 602/10/008, 261
 2 CURRENT FILING DATE: 2003-01-08
 3 PRIOR APPLICATION NUMBER: 60/276,709
 4 PRIOR FILING DATE: 2001-03-16
 5 NUMBER OF SEQ. TO NO.: 131066

```

1  NUMBER OF SEQ ID NOS: 13100
2
3  SOFTWARE: Microarray Probe Sequence Listing Generator V 1.0
4
5  SEQ ID NO 17109
6
7  LENGTH: 25
8
9  TYPE: DNA

```

TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-263B-17109

100

1. *Staphylococcus aureus*

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 19564
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-19564

Query Match: 48.9% Score 13.41 DB 15; Length 25;
 Best Local Similarity: 62.3% Pctd. No. 1.7e+04;
 Matches: 17; Conservative: 0; Mismatches: 8; Indels: 0; Gaps: 0;

CY 3 CTGAGCAATACCTAACGAAATA 25
 DB 25 CTGAGCAATACCTAACGAAATA 3

RESULT 14
 US-10-098-263B-19564
 Sequence: 19564, Application US/098263B
 Publication No. US20030007841A1
 GENERAL INFORMATION:
 APPLICANT: Mettler, Michael
 TITLE OF INVENTION: Human Milk
 FILE REFERENCE: 31481
 CURRENT FILING DATE: 1999-03-24
 PRIOR APPLICATION NUMBER: 09/0734061
 PRIOR FILING DATE: 1999-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: FASTASeq 1.1 Windows Version 4.0
 SEQ ID NO: 19564
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-19564

Query Match: 48.9% Score 13.41 DB 15; Length 25;
 Best Local Similarity: 62.3% Pctd. No. 1.7e+04;
 Matches: 17; Conservative: 0; Mismatches: 8; Indels: 0; Gaps: 0;

CY 5 GAGCATACCTAACGAAATA 22
 DB 25 GAGCATACCTAACGAAATA 8

RESULT 15
 US-09-894-793-17
 Sequence: 17, Application US/09894793
 Publication No. US20030007841A1
 GENERAL INFORMATION:
 APPLICANT: Mettler, Michael
 TITLE OF INVENTION: Human Milk
 FILE REFERENCE: 31481
 CURRENT FILING DATE: 1999-03-24
 PRIOR APPLICATION NUMBER: 09/0734061
 PRIOR FILING DATE: 1999-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: FASTASeq 1.1 Windows Version 4.0
 SEQ ID NO: 17
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:
 OTHER INFORMATION: oligonucleotide
 US-09-894-793-17

Query Match: 48.9% Score 13.41 DB 15; Length 30;
 Best Local Similarity: 62.3% Pctd. No. 1.7e+04;
 Matches: 15; Conservative: 0; Mismatches: 8; Indels: 0; Gaps: 0;

CY 1 TCCGAGCAATACCTAAC 18
 DB 9 TCCGAGCAATACCTAAC 26

RESULT 16
 US-10-095-906-179
 Sequence: 179, Application US/10085906
 Publication No. US20030054371A1
 GENERAL INFORMATION:
 APPLICANT: Ying, Vincent
 APPLICANT: Wu, Paul
 APPLICANT: Gray, Gary S.
 TITLE OF INVENTION: POLYMERASE CHAIN REACTION IN THE
 PRESENCE OF A POLYMERASE INHIBITOR
 FILE REFERENCE: GNN 534302
 CURRENT FILING DATE: 2002-02-27
 PRIOR APPLICATION NUMBER: 09/0734061
 PRIOR FILING DATE: 1999-03-25
 PRIOR FILING DATE: 1999-03-25
 PRIOR FILING DATE: 1999-03-25
 PRIOR FILING DATE: 1999-03-25
 NUMBER OF SEQ ID NOS: 545
 SOFTWARE: FASTASeq 1.1 Windows Version 4.0
 SEQ ID NO: 179
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-085-906-179

Query Match: 48.9% Score 13.41 DB 15; Length 30;
 Best Local Similarity: 62.3% Pctd. No. 1.7e+04;
 Matches: 18; Conservative: 0; Mismatches: 8; Indels: 0; Gaps: 0;

CY 2 CTGAGCAATACCTAACGAAATA 27
 DB 1 CCGCAGCAATACCTAACGAAATA 26

RESULT 17
 US-10-156-306-3091
 Sequence: 3091, Application US/10156306
 Publication No. US20030119017A1
 GENERAL INFORMATION:
 APPLICANT: Rhozyme Pharmaceuticals, Inc.
 APPLICANT: Rhozyme Pharmaceuticals, Inc.
 TITLE OF INVENTION: Enzymatic Method for Treatment of Disorders of Lipid Metabolism
 FILE REFERENCE: 31481
 CURRENT FILING DATE: 2002-03-24
 PRIOR APPLICATION NUMBER: 09/0734061
 PRIOR FILING DATE: 1999-03-16
 NUMBER OF SEQ ID NOS: 8013
 SOFTWARE: FASTASeq 1.1 Windows Version 4.0
 SEQ ID NO: 3091
 LENGTH: 31
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Enzymatic Nucleic Acid
 US-10-156-306-3091

Query Match: 48.9% Score 13.41 DB 15; Length 31;
 Best Local Similarity: 62.3% Pctd. No. 1.7e+04;
 Matches: 18; Conservative: 0; Mismatches: 8; Indels: 0; Gaps: 0;

CY 2 CTGAGCAATACCTAACGAAATA 27
 DB 5 CTGAGCAATACCTAACGAAATA 30

Match: 16, Conservative: 0, Mismatches: 7, Indels: 0, Gaps: 0.

27 1 TCGAGCATATCTTAAAGGACAA 23
|||||
7 TCAAGAGAGATCAATTAAGGACAA 31

RESULT 9

US-10-098-263B-18746
Sequence 18746, Application US/0003263B
Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/0003263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 00/0003263B

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 11006

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO: 3514

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-098-263B-3514

Query Match: 50.4%; Score 13.6; DB 15; Length 25;
Best Local Similarity: 80.0%; Pred. No. 1.1e+04;

Matches: 16; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

QY 1 TCGAGCATATCTTAAAGGACAA 23

|||||
23 TCGAGCATATCTTAAAGGACAA 4

|||||

RESULT 10

US-10-098-263B-18746

Sequence 18746, Application US/0003263B

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/0003263B

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 00/0003263B

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 11006

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

SEQ ID NO: 18746

LENGTH: 25

TYPE: DNA

ORGANISM: Homo sapiens

US-10-098-263B-18746

Query Match: 50.4%; Score 13.6; DB 15; Length 25;
Best Local Similarity: 80.0%; Pred. No. 1.1e+04;

Matches: 16; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

QY 4 TCGAGCATATCTTAAAGGACAA 23

|||||
1 TCGAGCATATCTTAAAGGACAA 20

|||||

RESULT 11

US-10-108-605-170

Sequence 170, Application US/0108605

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Miltman, Michael

TITLE OF INVENTION: Human Microarray

FILE REFERENCE: 3118.1

CURRENT APPLICATION NUMBER: US/0108605

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: 00/0003263B

PRIOR FILING DATE: 2001-03-16

NUMBER OF SEQ ID NOS: 11006

SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1

APPLICANT: Kamdar, Kim

TITLE OF INVENTION: METHOD AND APPARATUS FOR PROVIDING A HUMAN MICROARRAY THAT INCLUDES

FILE REFERENCE: 31133B

CURRENT APPLICATION NUMBER: US/0108605

CURRENT FILING DATE: 2003-01-08

PRIOR APPLICATION NUMBER: US/00761142

PRIOR FILING DATE: 2001-01-16

NUMBER OF SEQ ID NOS: 114

SOFTWARE: Patent In Vitro 2.1

SEQ ID NO: 1

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence, File 11006

US-10-108-605-1

Query Match: 50.4%; Score 13.6; DB 15; Length 27;
Best Local Similarity: 80.0%; Pred. No. 1.1e+04;

Matches: 16; Conservative: 0; Mismatches: 4; Indels: 0; Gaps: 0;

QY 4 TCGAGCATATCTTAAAGGACAA 23

|||||
23 TCGAGCATATCTTAAAGGACAA 3

|||||

RESULT 12

US-10-215-112-5782/c

Sequence 5782, Application US/0215112

Publication No. US20030104410A1

GENERAL INFORMATION:

APPLICANT: Michael Miltman

TITLE OF INVENTION: Method of Genetic Analysis of Proteins

FILE REFERENCE: 3113

CURRENT APPLICATION NUMBER: US/0215112

CURRENT FILING DATE: 2002-08-08

NUMBER OF SEQ ID NOS: 14936

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO: 5782

LENGTH: 25

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic Oligonucleotide

US-10-215-112-5782

Query Match: 49.6%; Score 13.4; DB 15; Length 25;
Best Local Similarity: 73.0%; Pred. No. 1.4e+04;

Matches: 17; Conservative: 0; Mismatches: 6; Indels: 0; Gaps: 0;

QY 2 CTTGAGCATATCTTAAAGGACAA 24

|||||
25 CTTGAGCATATCTTAAAGGACAA 3

|||||

01-09 065-272 248

SEQUENCE INFORMATION: CIG 12 NO. 018

1 SOFTWARE: ASCII TEXT
2
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: 63/067966-271
5
6 FILING DATE: 22 Jan. 2001
7
8 CLASSIFICATION: <UNKNOWN>
9
10 PRIORITY APPLICATION DATA:
11 APPLICATION NUMBER: 08/061063
12
13 FILING DATE: <UNKNOWN>
14
15 ATTORNEY/AGENT INFORMATION:
16 NAME: BLOOMER, A. ANDRES
17 REGISTRATION NUMBER: 36 303 4712
18
19 REFERENCE/RELATED NUMBER: 1537711
20
21 TELECOMMUNICATION INFORMATION:
22 TELEPHONE: (301) 305-8504
23
24 TELEFAX: (301) 309-8512
25
26 INFORMATION FOR SEQ. ID. 1:
27
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 35 base pairs
30 TYPE: nucleic acid
31 STRATEGY: J, L11
32 TOPOLOGY: linear
33
34 SEQUENCE INFORMATION: CIG 12 NO. 018

Query Matrix	Seq. ID	Score	E-Value	Length
Best Local Similarity	58.8%	300.0	1.9e-03	100
Best Local Similarity	79.2%	Prod. No.	2.0e+03	
Matches 18	Conservation	Widely	Has	

27	CGGCTAAATGCTGTAACGAGGCGGAAATG	27
28	CTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT	28
29	GACCAATACCTGCTGCGGAGGAGGAGGAGG	29

```

RESULT 5
CS-10-0904 263R-86094/C
Sequence: 20714, 44714, 114714, 174714
Publication No. 0326031044101
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 311R
CURRENT AFFILIATION: NIMBLE, 0326031044101, 463B
CURRENT FILING DATE: 2003-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIOR FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1.1
SEQ ID NO: 86094
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
IS-10-0904-263R-86094

```

	Query Match	51.0%	Score 14	ED 15	Length 25
	Percent Identity	100.0%	Pos 14	7	4.0%
Matches	14	Conservative	0	Mismatches	0
	14	CTAAGACACAAATA	27		
QY	14	CTAAGACACAAATA	27		
	14		14		
db	15	CTAAGACACAAATA	2		

RESULT 6
 US 10-098-263B 11078/C
 Sequence 118978, Application No 10009052B
 Publication No 1000020104401
 GENERAL INFORMATION:
 APPLICANT: MURPHY, W. H. J.
 FILE OR INVENTION: Great Britain
 FILE REFERENCE: 11818
 CURRENT APPLICATION NUMBER: 10009052B
 CURRENT FILING DATE: 2002.01.08
 PRIORITY APPLICATION NUMBER: 00107673

PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ. IDS: 134066
 SOFTWARE: MCL-PROTEOMICS FILE-TO-FASTA CONVERTER V 1.0
 SEQ ID NO: 118678
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 OS-10-098 263B-118078

DATE RECEIVED	AMOUNT	PAID	DEPOSIT	MONTH
1900-1-1	100.00	50.00	50.00	1
1900-1-15	200.00	100.00	100.00	1
1900-1-30	300.00	150.00	150.00	1
1900-2-1	400.00	200.00	200.00	2
1900-2-15	500.00	250.00	250.00	2
1900-2-28	600.00	300.00	300.00	2
1900-3-1	700.00	350.00	350.00	3
1900-3-15	800.00	400.00	400.00	3
1900-3-31	900.00	450.00	450.00	3
1900-4-1	1000.00	500.00	500.00	4
1900-4-15	1100.00	550.00	550.00	4
1900-4-30	1200.00	600.00	600.00	4
1900-5-1	1300.00	650.00	650.00	5
1900-5-15	1400.00	700.00	700.00	5
1900-5-31	1500.00	750.00	750.00	5
1900-6-1	1600.00	800.00	800.00	6
1900-6-15	1700.00	850.00	850.00	6
1900-6-30	1800.00	900.00	900.00	6
1900-7-1	1900.00	950.00	950.00	7
1900-7-15	2000.00	1000.00	1000.00	7
1900-7-31	2100.00	1050.00	1050.00	7
1900-8-1	2200.00	1100.00	1100.00	8
1900-8-15	2300.00	1150.00	1150.00	8
1900-8-31	2400.00	1200.00	1200.00	8
1900-9-1	2500.00	1250.00	1250.00	9
1900-9-15	2600.00	1300.00	1300.00	9
1900-9-30	2700.00	1350.00	1350.00	9
1900-10-1	2800.00	1400.00	1400.00	10
1900-10-15	2900.00	1450.00	1450.00	10
1900-10-31	3000.00	1500.00	1500.00	10
1900-11-1	3100.00	1550.00	1550.00	11
1900-11-15	3200.00	1600.00	1600.00	11
1900-11-30	3300.00	1650.00	1650.00	11
1900-12-1	3400.00	1700.00	1700.00	12
1900-12-15	3500.00	1750.00	1750.00	12
1900-12-31	3600.00	1800.00	1800.00	12

G7		1	TGCTGGCAATACCTTAAGAAC	2
U6		24	UGTGAACACAACTAATTAC	3

```

RESULT 7
US:10 008 463b-41030/C
Sequence 41030, Annotation US:700000026B
FullAccess NO, Accession 001044101
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 318,113
OFFICE ATTORNEY: JENNIFER L. WILSON, 1001-102-1018
CURRENT FILING DATE: 2003-01-08
FILER ATTORNEY: JENNIFER L. WILSON, 1001-102-1018
PRIORITY DATE: 2001-03-16
NUMBER OF SEQ. ID NOS.: 14000
SOFTWARE: Microarray Slice Scanner Listing Generator V 1.1
SEQ ID NO. 41030
LENGTH: 25
TYPE: DNA
ORIGIN: Homo sapiens
US:10 008 463b-41030

```

[illegible]

RESULT B
HS-09-918-036-15

```

GENERAL INFORMATION:
APPLICANT: MADURA, Kiran
FILE OF INVENTION: M14-00 AND 159-00000 FOR THE PATENT IDENTIFICATION
FILE OF INVENTION: M14-00 AND 159-00000 FOR THE PATENT IDENTIFICATION
FILE REFERENCE: 066/16599
CURRENT APPLICATION NUMBER: 03/09/918.036
CURRENT FILING PATH: 2001-06-10
PRIORITY APPLICATION NUMBER: 03/09/918.036
PRIORITY FILING DATE: 1997-06-19
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 15
LENGTH: 32
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 159-00000 FOR THE PATENT IDENTIFICATION
OTHER INFORMATION: 159-00000 FOR THE PATENT IDENTIFICATION
IS-09-918-036-15

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C 966 10.2 17.8 25 15 US-10-098-2638-44086 Sequence 81986, A
C 967 10.2 17.8 25 15 US-10-098-2638-44012 Sequence 44012, A
C 968 10.2 17.8 25 15 US-10-098-2638-44016 Sequence 44016, A
C 969 10.2 17.8 25 15 US-10-098-2638-44017 Sequence 44017, A
C 970 10.2 17.8 25 15 US-10-098-2638-44018 Sequence 44018, A
C 971 10.2 17.8 25 15 US-10-098-2638-44019 Sequence 44019, A
C 972 10.2 17.8 25 15 US-10-098-2638-44020 Sequence 44020, A
C 973 10.2 17.8 25 15 US-10-098-2638-44021 Sequence 44021, A
C 974 10.2 17.8 25 15 US-10-098-2638-44022 Sequence 44022, A
C 975 10.2 17.8 25 15 US-10-098-2638-44023 Sequence 44023, A
C 976 10.2 17.8 25 15 US-10-098-2638-44024 Sequence 44024, A
C 977 10.2 17.8 25 15 US-10-098-2638-44025 Sequence 44025, A
C 978 10.2 17.8 25 15 US-10-098-2638-44026 Sequence 44026, A
C 979 10.2 17.8 25 15 US-10-098-2638-44027 Sequence 44027, A
C 980 10.2 17.8 25 15 US-10-098-2638-44028 Sequence 44028, A
C 981 10.2 17.8 25 15 US-10-098-2638-44029 Sequence 44029, A
C 982 10.2 17.8 25 15 US-10-098-2638-44030 Sequence 44030, A
C 983 10.2 17.8 25 15 US-10-098-2638-44031 Sequence 44031, A
C 984 10.2 17.8 25 15 US-10-098-2638-44032 Sequence 44032, A
C 985 10.2 17.8 25 15 US-10-098-2638-44033 Sequence 44033, A
C 986 10.2 17.8 25 15 US-10-098-2638-44034 Sequence 44034, A
C 987 10.2 17.8 25 15 US-10-098-2638-44035 Sequence 44035, A
C 988 10.2 17.8 25 15 US-10-098-2638-44036 Sequence 44036, A
C 989 10.2 17.8 25 15 US-10-098-2638-44037 Sequence 44037, A
C 990 10.2 17.8 25 15 US-10-098-2638-44038 Sequence 44038, A
C 991 10.2 17.8 25 15 US-10-098-2638-44039 Sequence 44039, A
C 992 10.2 17.8 25 15 US-10-098-2638-44040 Sequence 44040, A
C 993 10.2 17.8 25 15 US-10-098-2638-44041 Sequence 44041, A
C 994 10.2 17.8 25 15 US-10-098-2638-44042 Sequence 44042, A
C 995 10.2 17.8 25 15 US-10-098-2638-44043 Sequence 44043, A
C 996 10.2 17.8 25 15 US-10-098-2638-44044 Sequence 44044, A
C 997 10.2 17.8 25 15 US-10-098-2638-44045 Sequence 44045, A
C 998 10.2 17.8 25 15 US-10-098-2638-44046 Sequence 44046, A
C 999 10.2 17.8 25 15 US-10-098-2638-44047 Sequence 44047, A

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ALIGNMENTS

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RESULT 1
US-10-098-2638-115419/C
Sequence 115419, Affiliation: US-10-098-2638
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 2638
PRIORITY FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 115419
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2638-115419

Query Match: 58.6% Score 151 DB 151 Length 25
Best Local Similarity: 91.9% Prod No. 150-033
Matches: 18; Conservative: 9; Mismatches: 4; Indels: 0; Gaps: 0;

4 TAGAGTATACCTAGGACAA 25
|||||
25 TAGAGTATACCTAGGACAA 4

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RESULT 2
US-10-098-2638-115420/C
Sequence 115420, Affiliation: US-10-098-2638
Publication No. US20030104410A1

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GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 2638
PRIORITY FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 115420
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2638-115420

Query Match: 58.6% Score 151 DB 151 Length 25
Best Local Similarity: 91.9% Prod No. 150-033
Matches: 18; Conservative: 9; Mismatches: 4; Indels: 0; Gaps: 0;

4 TAGAGTATACCTAGGACAA 25
|||||
25 TAGAGTATACCTAGGACAA 4

RESULT 3
US-10-098-2638-115421/C
Sequence 115421, Affiliation: US-10-098-2638
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 2638
PRIORITY FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 115421
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2638-115421

Query Match: 58.6% Score 151 DB 151 Length 25
Best Local Similarity: 91.9% Prod No. 150-033
Matches: 18; Conservative: 9; Mismatches: 4; Indels: 0; Gaps: 0;

4 TAGAGTATACCTAGGACAA 25
|||||
25 TAGAGTATACCTAGGACAA 4

RESULT 4
US-10-098-2638-115422/C
Sequence 115422, Affiliation: US-10-098-2638
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098, 2638
PRIORITY FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-01-08
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V.1.1
SEQ ID NO 115422
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-098-2638-115422

Query Match: 58.6% Score 151 DB 151 Length 25
Best Local Similarity: 91.9% Prod No. 150-033
Matches: 18; Conservative: 9; Mismatches: 4; Indels: 0; Gaps: 0;

4 TAGAGTATACCTAGGACAA 25
|||||
25 TAGAGTATACCTAGGACAA 4

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44M
COMPILED BY: WJL/10/098-2638-115422
OPERATING SYSTEM: MS-DOS 6.22

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100

17	13	48.9	81	15	08-10-15b-00b-1001	Sequence 17, Apr
16	12	48.1	82	12	08-10-15b-00b-1001	Sequence 16, Apr
15	11	48.1	83	12	08-10-15b-00b-1001	Sequence 15, Apr
14	10	48.1	84	12	08-10-15b-00b-1001	Sequence 14, Apr
13	9	48.1	85	15	08-10-15b-00b-1001	Sequence 13, Apr
12	8	48.1	86	15	08-10-15b-00b-1001	Sequence 12, Apr
11	7	48.1	87	15	08-10-15b-00b-1001	Sequence 11, Apr
10	6	48.1	88	15	08-10-15b-00b-1001	Sequence 10, Apr
9	5	48.1	89	15	08-10-15b-00b-1001	Sequence 9, Apr
8	4	48.1	90	15	08-10-15b-00b-1001	Sequence 8, Apr
7	3	48.1	91	15	08-10-15b-00b-1001	Sequence 7, Apr
6	2	48.1	92	15	08-10-15b-00b-1001	Sequence 6, Apr
5	1	48.1	93	15	08-10-15b-00b-1001	Sequence 5, Apr
4	0	48.1	94	15	08-10-15b-00b-1001	Sequence 4, Apr
3	0	48.1	95	15	08-10-15b-00b-1001	Sequence 3, Apr
2	0	48.1	96	15	08-10-15b-00b-1001	Sequence 2, Apr
1	0	48.1	97	15	08-10-15b-00b-1001	Sequence 1, Apr

APPLICANT: Chung, Ming Yi
APPLICANT: Zeng, Hui Y.
TITLE OF INVENTION: Gene Sequence for Spinothalamic Ataxia
Patent No. 6834183
TITLE OF INVENTION: Type 1 and Method for Diagnosis
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESS: Meeting, P.O. Box 581415
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55458-1415
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPILED BY: IBM PC compatible
CREATING SYSTEM: PC DOS 5.0
SOFTWARE: IBM PC Release #1.0, Version #1.0
CURRENT APPLICATION DATA
APPLICATION NUMBER: US/89/03638
FILING DATE: 29 JUN 1994
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: McCormack, Myra H.
REGISTRATION NUMBER: 36,602
REFERENCE/AGENT INFORMATION:
TELEPHONE: 612-305-1217
TELEFAX: 612-305-1224
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US 09-890-363-4
Query Match
Best Local Similarity 45.24, Score 12.41, DB 1, Length 28:
Matches 16, Conservative 0, Mismatches 6, Indels 0, Gaps 0

1 TOTGAGCAATGCTAACGAC 22
1 TOTGAGCAATGCTAACGAC 22
Db
RESULT 40
US/89/03638-124A-326/0
Sequence 326, Application US/89/03638-124A
Patent No. 5646042
GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: Madsen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TITLE OF INVENTION: TREATMENT OF PTERYGIOS AND
TITLE OF INVENTION: CANCER USING FIBROBLASTS
NUMBER OF SEQUENCES: 327
CORRESPONDENCE ADDRESS:
ADDRESS: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: Storage
COMPILED BY: IBM Compatible
CREATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/245,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 08/170,948
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07/987,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07/516,422
FILING DATE: August 26, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard
REGISTRATION NUMBER: 32,327
REFERENCE/AGENT INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 326:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-373-124A-326
Query Match
Best Local Similarity 82.44, Score 12.21, DB 1, Length 17:
Matches 14, Conservative 0, Mismatches 3, Indels 0, Gaps 0

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-890-363-4

Query Match 45.9% Score 12.4; DB 3; Length 19;
 Best local similarity 92.9% (id: 1); Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

3 CTGAGCAATACCTA 16
 5 CTGAGCAATACCTA 18

RESULT 36
 US-09-890-363-4
 Sequence 11: Application US/09/070964
 Patent No. 6017730
 GENERAL INFORMATION:
 APPLICANT: MOLIN, SOREN
 APPLICANT: GISKOV, MICHAEL
 APPLICANT: KRISTENSEN, CLAUD S
 APPLICANT: BERG, ASIM K
 APPLICANT: EBERL, LEO
 TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF
 TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Broadway and Newmark
 STREET: 419 Seventh St., N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States of America
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 13-OCT-1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/115,065
 FILING DATE: 13-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: MOLIN-6A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 628 5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (synthetic)
 US-09-890-363-4

Query Match 45.9% Score 12.4; DB 3; Length 19;
 Best local similarity 92.9% (id: 1); Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

3 CTGAGCAATACCTA 16
 15 CTGAGCAATACCTA 2

RESULT 37
 US-09-890-363-4
 Sequence 11: Application US/09/070964
 Patent No. 6017730
 GENERAL INFORMATION:
 APPLICANT: MOLIN, SOREN
 APPLICANT: GISKOV, MICHAEL
 APPLICANT: KRISTENSEN, CLAUD S
 APPLICANT: BERG, ASIM K
 APPLICANT: EBERL, LEO
 TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF
 TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Broadway and Newmark
 STREET: 419 Seventh St., N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States of America
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 13-OCT-1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/115,065
 FILING DATE: 13-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: MOLIN-6A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 628 5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-890-363-4

Query Match 45.9% Score 12.4; DB 3; Length 19;
 Best local similarity 92.9% (id: 1); Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

3 CTGAGCAATACCTA 16
 5 CTGAGCAATACCTA 18

RESULT 38
 US-09-890-363-4
 Sequence 11: Application US/09/070964
 Patent No. 6017730
 GENERAL INFORMATION:
 APPLICANT: MOLIN, SOREN
 APPLICANT: GISKOV, MICHAEL
 APPLICANT: KRISTENSEN, CLAUD S
 APPLICANT: BERG, ASIM K
 APPLICANT: EBERL, LEO
 TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF
 TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Broadway and Newmark
 STREET: 419 Seventh St., N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: United States of America
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 FILING DATE: 13-OCT-1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/115,065
 FILING DATE: 13-OCT-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: COOPER, IVER P
 REGISTRATION NUMBER: 28,005
 REFERENCE/DOCKET NUMBER: MOLIN-6A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 628 5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-890-363-4

Query Match 45.9% Score 12.4; DB 3; Length 19;
 Best local similarity 92.9% (id: 1); Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patulin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/07/448,604

FILING DATE: 27 NO. 631203 1993

CLASSIFICATION: unknown

07-APR-1996

24 JUN 1994

Prior Application Data:

APPLICATION NUMBER: 08/757,347

FILING DATE: unknown

APPLICATION NUMBER: 08/992,934,0

FILING DATE: 07-APR-1996

APPLICATION NUMBER: 08/448,016,5

FILING DATE: 24 JUN 1994

ATTORNEY/AGENT INFORMATION:

NAME: CASOFF, B.C.

REGISTRATION NUMBER: 36,663

REFERENCE/DOCKET NUMBER: 149 / 14

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4091

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 30 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

HYDROTHERMAL: NO

ANTI SENSE: NO

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-448-804 53

Query Match 46.73; Score 12.6; DB: 4; Length 30;

Best Local Similarity: 66.78; Freq: No. 2 44.00;

Matches: 18; Conservative: 0; Mismatches: 9; Indels: 0; Gaps: 0;

CY 1 TCTGAGCAATACCTAAGCAATAAATA 27

DB 1 TAGCAATCAAAATCAATCAATCAATCA 27

RESULT 34

US-08-544-822-10/2

Sequence 11, Application US/08544822

Patent No. 5834233

GENERAL INFORMATION:

APPLICANT: MOLIN, Soren

APPLICANT: GISOV, Michael

APPLICANT: KRISTENSEN, Claus S

APPLICANT: BEJ, Asim K

APPLICANT: EBERL, Leo

TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF

TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR

NUMBER OF SEQUENCES: 14

REFERENCE ADDRESS:

ADDRESSER: Broadway and Newark

STREET: 419 Seventh St., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patulin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/135,665

FILING DATE: 13 October 1993

Prior Application Data:

APPLICATION NUMBER: 08/135,665

FILING DATE: 13 October 1993

Prior Application Data:

APPLICATION NUMBER: 07/503,261

FILING DATE: 06 April 1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P

REGISTRATION NUMBER: 29,005

REFERENCE/DOCKET NUMBER: MOLIN-68

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-679-0197

TELEFAX: 202-737-1928

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

US-08-544-822-10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/081,444,822

FILING DATE: 18 October 1995

Prior Application Data:

APPLICATION NUMBER: 08/135,665

FILING DATE: 13 October 1993

Prior Application Data:

APPLICATION NUMBER: 07/503,261

FILING DATE: 06 April 1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P

REGISTRATION NUMBER: 29,005

REFERENCE/DOCKET NUMBER: MOLIN-68

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-679-0197

TELEFAX: 202-737-1928

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (synthetic)

US-08-544-822-10

Query Match 45.93; Score 12.4; DB: 2; Length 19;

Best Local Similarity: 92.08; Freq: No. 2 96.03;

Matches: 13; Conservative: 0; Mismatches: 1; Indels: 0; Gaps: 0;

CY 3 CTGAGCAATACCTA 16

DB 15 CTGAGCAATACCTA 2

RESULT 35

US-08-544-822-11

Sequence 11, Application US/08544822

Patent No. 5834233

GENERAL INFORMATION:

APPLICANT: MOLIN, Soren

APPLICANT: GISOV, Michael

APPLICANT: KRISTENSEN, Claus S

APPLICANT: BEJ, Asim K

APPLICANT: EBERL, Leo

TITLE OF INVENTION: A METHOD OF LIMITING THE SURVIVAL OF

TITLE OF INVENTION: GENETICALLY ENGINEERING MICROORGANISMS IN THEIR

NUMBER OF SEQUENCES: 14

REFERENCE ADDRESS:

ADDRESSER: Broadway and Newark

STREET: 419 Seventh St., N.W.

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patulin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 08/135,665

FILING DATE: 13 October 1993

Prior Application Data:

APPLICATION NUMBER: 08/135,665

FILING DATE: 13 October 1993

Prior Application Data:

APPLICATION NUMBER: 07/503,261

FILING DATE: 06 April 1992

ATTORNEY/AGENT INFORMATION:

NAME: COOPER, Iver P

REGISTRATION NUMBER: 29,005

REFERENCE/DOCKET NUMBER: MOLIN-68

```

1 TITLE OF INVENTION: AGE DIFFERENTIATION OF FORESTRIFT DATA USING A
2 HYPERTEXT-DRIVEN HYPERMEDIATION ASSAY
3 NUMBER OF SEQUENCES: 216
4 CORRESPONDENCE ADDRESS:
5 ADDRESSEE: NIXON & VANDERHIVE P.C.
6 STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
7 CITY: WASHINGTON
8 STATE: D.C.
9 COUNTRY: USA
10 ZIP: 22201
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: 1.02/2.04/MS-DOS
16 SOFTWARE: Forensic Release #1.0, Version #1.0
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/82/765,332
19 FILING DATE: 23-DEC-1996
20 CLASSIFICATION: 435
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: W3 PCT/EP/95/02152
24 FILING DATE: 03 JUN 1995
25
26 PRIOR APPLICATION DATA:
27 APPLICATION NUMBER: EP 698/1032.0
28 FILING DATE: 07-APR-1995
29
30 PRIOR APPLICATION DATA:
31 APPLICATION NUMBER: EP 948/0106.5
32 FILING DATE: 24 JUN-1994
33
34 ATTORNEY/AGENT: JF-PHARMATON
35 NAME: SAUOFF, B. J.
36
37 REGISTRATION NUMBER: 35,653
38 REFERENCE/SECRET NUMBER: 1487-14
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: 703-816-4101
41 TELEFAX: 703-816-4100
42
43 INFORMATION FOR CLASSIFICATION: 53:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 50 base pairs
46 TYPE: nucleic acid
47 STRANDEDNESS: single
48 TOPOLOGY: linear
49
50 MULTIPLE TYP: CINA
51 HYPOTHEICAL: NO
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53 ANTI GENSE: NO
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RESULT 28
US-09-446-047A 9/c
Sequence 9, Application US/09446047A
Patent No. 6179924

GENERAL INFORMATION:

APPLICANT: Darrill Sleep
Delta Biotechnology Limited
TITLE OF INVENTION: Improved Protein Expression Strains
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Aventis Behring LLC
STREET: 1020 First Avenue
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: United States of America
ZIP: 19406-1316

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/446-047A
FILING DATE: 15-Dec-1999

SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE ID: 511709 14 11 3 4

US-09 446-047A-9

Query Match

Best local similarity: 47.4% Score 12.6 DB 4: Length 33;
Mismatch 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 TTTTAACTAAGCAATAATA 24
DB 29 TTTTAACTAAGCAATAATA 6

FIGURE 29
US-09-311-311C-4
Sequence 4, Application US/0931111C
Patent No. 6182738

GENERAL INFORMATION:

APPLICANT: Erikson, et al
TITLE OF INVENTION: POLY-BAX THERAPEUTIC COMPOSITIONS,
FILE REFERENCE: 1874/117
CURRENT APPLICATION NUMBER: US/09/311-311C
CURRENT FILING DATE: 1999-05-13
PRIORITY APPLICATION NUMBER: US/01/065,136
PRIORITY FILING DATE: 1998-05-13
NUMBER OF SEQ TO NOS: 27
SOFTWARE: Pasteraq for Windows Version 4.0
SEQ ID NO: 4

LENGTH: 26

TYPE: DNA

ORGANISM: PCR primer

FIGURE: 1

US-09-311-311C-4

Query Match: 46.7% Score 12.6 DB 4: Length 26;
Best local similarity: 79.2% Freq. No. 2,36,031;
Mismatch 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 9 AATACTAAGCAATAATA 27
DB 6 AATACTAAGCAATAATA 24

RESULT 30
US-08-664-040-4694

Sequence 4694, Application US/08040404
Patent No. 6346398

GENERAL INFORMATION:

APPLICANT: Favco, Pamela
ADDRESSEE: McGivern, James
APPLICANT: Slinchcomb, Dan T.
APPLICANT: Escobedo, Jaime
TITLE OF INVENTION: METHOD AND REAGENT FOR THE
TITLE OF INVENTION: TREATMENT OF DISEASES OF
TITLE OF INVENTION: GENITING RELATED TO LEVELS
TITLE OF INVENTION: OF VAGINAR PHOTOPHILIA
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 9502
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB
MEDIUM TYPE: Storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM EBC 200 0.0
SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/664-040
FILING DATE: January 11, 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 6/000,974
FILING DATE: October 26, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 218/064

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1609
TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NOS: 4694:

SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDNESS: single
TOPOLOGY: linear

FEATURE:

OTHER INFORMATION: The letter 'm' represents the base 11 position
of an mRNA library.

US-08-664-040-4694

Query Match: 46.7% Score 12.6 DB 4: Length 27;
Best local similarity: 65.0% Freq. No. 2,36,031;
Mismatch 19; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 AGCAATACATAGCAATAA 26
DB 1 AGCAATACATAGCAATAA 20

RESULT 31
US-08-679-045-1602
Sequence 1602, Application US/080451602
Patent No. 6160934

ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORESTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MO
 COUNTRY: USA
 ZIP: 63105

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/118,626
 FILING DATE:

CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 871486
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 314 727 5188
 TELEFAX: 314-727-6092

INFORMATION FOR SEQ ID NO: 145:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 US-09-891 859E 145

Query Match 47.4% Score 12.87 DB 4 Length 25
 Best Local Similarity 97.5% Pred. No. 119e+03
 Matched 14, Conserved 9, Mismatches 2, Indels 0, Gaps 0

21 CTGAGCAATACCTAGC 6

RESULT 26
 US-09-891-739-145/C
 Sequence 145, Application US/09091739
 Patent No. 6232449
 GENEPAT INFORMATION:
 APPLICANT: JOHNSON OF, THOMAS M.
 MILBRANDT, JEFFREY D.
 KOTZBAUER, PAUL T.
 LAMPE, PATRICIA A.
 TITLE OF INVENTION: HEPATITIS AND RELATED DISEASES
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORESTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/118,626
 FILING DATE: 31-Aug-1998
 CLASSIFICATION: 435, 436, 437

PRICE APPLICATION DATA:
 APPLICATION NUMBER: 717/093 118626
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197

REFERENCE/DOCKET NUMBER: 976103
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 145:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 SEQUENCE INFORMATION: SEQ ID NO: 145:
 US-09-891-739-145

Query Match 47.4% Score 12.87 DB 4 Length 25
 Best Local Similarity 97.5% Pred. No. 119e+03
 Matched 14, Conserved 9, Mismatches 2, Indels 0, Gaps 0

21 CTGAGCAATACCTAGC 6

RESULT 27
 US-09-128-026-145/C
 Sequence 145, Application US/09128026
 Patent No. 6403315

GENERAL INFORMATION:
 APPLICANT: JOHNSON OF, THOMAS M.
 MILBRANDT, JEFFREY D.
 KOTZBAUER, PAUL T.
 LAMPE, PATRICIA A.
 TITLE OF INVENTION: HEPATITIS AND RELATED DISEASES
 NUMBER OF SEQUENCES: 176
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HOWELL & HAFERKAMP, L.C.
 STREET: 7733 FORESTH BOULEVARD, SUITE 1400
 CITY: ST. LOUIS
 STATE: MISSOURI
 COUNTRY: US
 ZIP: 63105-1817

COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/118,626
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: HOLLAND, DONALD R.
 REGISTRATION NUMBER: 35,197
 REFERENCE/DOCKET NUMBER: 976103
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (314) 727-5188
 TELEFAX: (314) 727-6092

INFORMATION FOR SEQ ID NO: 145:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 25 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 US-09-128-026-145

Query Match 47.4% Score 12.87 DB 4 Length 25
 Best Local Similarity 97.5% Pred. No. 119e+03
 Matched 14, Conserved 9, Mismatches 2, Indels 0, Gaps 0

21 CTGAGCAATACCTAGC 6

APPLICATION NUMBER: 05/08/482,182
 FILING DATE: 07 JUN 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.
 REGISTRATION NUMBER: 35,636
 REFERENCE/INVENTOR NUMBER: 2004, 2004, 2004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 811-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 20:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-482,182-20

Query Match 47.4% Score 12.8; DP 2; Length 20;
 Best Local Similarity 87.5%, from NO. 1,840,03;
 Matches 14; Conservative 0, Mismatches 2, Indels 0, Gaps 0.

QY 3 CTGACCATACCTAAC 18
 17 CTGACCATACCTAAC 2

RESULT 21
 US-08-482,182-21
 Sequence 63, Application US/08482182
 Patent No. 5861273
 GENERAL INFORMATION:
 APPLICANT: MASTAFERRA, TESSA
 ATTORNEY/AGENT INFORMATION:
 NAME: OLSON, PAMELA S.
 REGISTRATION NUMBER: 37,029
 REFERENCE/INVENTOR NUMBER: 2004, 2004, 2004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 765 749-1111
 TELEFAX: 765 749-1111
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304 1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS 5.0
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/08/482,182
 FILING DATE: 07 JUN 1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.
 REGISTRATION NUMBER: 35,636
 REFERENCE/INVENTOR NUMBER: 2004, 2004, 2004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 811-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 63:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-482,182-63

Query Match 47.4% Score 12.8; DP 2; Length 20;
 Best Local Similarity 87.5%, from NO. 1,840,03;
 Matches 14; Conservative 0, Mismatches 2, Indels 0, Gaps 0.

QY 3 CTGACCATACCTAAC 18
 17 CTGACCATACCTAAC 2

RESULT 24
 US-08-445,289B-23
 Sequence 23, Application US/08445289B
 Patent No. 5693467
 GENERAL INFORMATION:
 APPLICANT: ROLLIN, III, Richard O.
 ATTORNEY/AGENT INFORMATION:
 NAME: Tang, Jane S.
 REGISTRATION NUMBER: 37,029
 REFERENCE/INVENTOR NUMBER: 2004, 2004, 2004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-816-4466
 TELEFAX: 310-816-4466
 CITY: Rockville
 STATE: Maryland
 COUNTRY: U.S.A.
 ZIP: 20852
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS 5.0
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/08/445,289B
 FILING DATE: 12-MAY-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: BADE, ANNETTE L.
 REGISTRATION NUMBER: 37,029
 REFERENCE/INVENTOR NUMBER: 2004, 2004, 2004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-231-5520
 TELEFAX: 301-231-5520
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-445,289B-23

Query Match 47.4% Score 12.8; DP 1; Length 21;
 Best Local Similarity 87.5%, from NO. 1,840,03;
 Matches 14; Conservative 0, Mismatches 2, Indels 0, Gaps 0.

QY 4 CTGACCATACCTAAC 19
 5 CTGACCATACCTAAC 20

RESULT 25
 US-08-931-858E-14E/C
 Sequence 14E, Application US/08931858E
 Patent No. 6,220,002
 GENERAL INFORMATION:
 APPLICANT: JOHNSON, EUGENE M.
 ATTORNEY/AGENT INFORMATION:
 NAME: MURRAY, JEFFREY D.
 REGISTRATION NUMBER: 37,029
 REFERENCE/INVENTOR NUMBER: 2004, 2004, 2004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-816-4466
 TELEFAX: 310-816-4466
 CITY: Rockville
 STATE: Maryland
 COUNTRY: U.S.A.
 ZIP: 20852
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS 5.0
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/08/931,858E
 FILING DATE: 12-MAY-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURRAY, JEFFREY D.
 REGISTRATION NUMBER: 37,029
 REFERENCE/INVENTOR NUMBER: 2004, 2004, 2004
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 310-816-4466
 TELEFAX: 310-816-4466
 INFORMATION FOR SEQ ID NO: 14E:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-931-858E-14E/C

INFORMATION FOR SEQ ID NO: 18
 SEQUENCE CHARACTERISTICS:
 LENGTH: 19 bases
 TYPE: Nucleic acid
 STRANDEDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: 17 terminal bases
 HYPOTHEICAL: NO
 ANTI GENE: Yes
 PRT-0896-05611A 18
 Query Match 47.4%, Score 12.87, DB 57, Length 197
 Best Local Similarity 97.8%, Pval: No. 1.9e-03
 Matches 14, Conservation 0, Mismatches 2, Indels 0, Gaps 0
 CY 1 CTGAGCAATACCTAAC 18
 DB 16 CTGAGCAATACCTAGC 1
 RESULT 20
 US-08-170-688-6/0
 Sequence 6, Application US/08/08421182
 Patent No. 5470727
 GENERAL INFORMATION:
 APPLICANT: MACCARENAS, DESMOND
 APPLICANT: OLSON, PAMELA S.
 TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
 TITLE OF INVENTION: GENES IN PATERNAL CHRIS
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/170,598
 FILING DATE: 21 DEC 1993
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.
 REGISTRATION NUMBER: 35,636
 REFERENCE/DOC# NUMBER: 22995-20291.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 913-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-170-588-6
 Query Match 47.4%, Score 12.87, DB 57, Length 20
 Best Local Similarity 97.8%, Pval: No. 1.9e-03
 Matches 14, Conservation 0, Mismatches 2, Indels 0, Gaps 0
 CY 3 CTGAGCAATACCTAAC 18
 DB 17 CTGAGCAATACCTAGC 2
 RESULT 21

US-08-170-182-6/0
 Sequence 6, Application US/08/08421182
 Patent No. 5861273
 GENERAL INFORMATION:
 APPLICANT: MACCARENAS, DESMOND
 APPLICANT: OLSON, PAMELA S.
 TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
 TITLE OF INVENTION: GENES IN PATERNAL CHRIS
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/482,182
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: PARK, FREDDIE K.
 REGISTRATION NUMBER: 35,636
 REFERENCE/DOC# NUMBER: 22995-20291.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 913-5600
 TELEFAX: (415) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-482-182-6
 Query Match 47.4%, Score 12.87, DB 57, Length 20
 Best Local Similarity 97.8%, Pval: No. 1.9e-03
 Matches 14, Conservation 0, Mismatches 2, Indels 0, Gaps 0
 CY 3 CTGAGCAATACCTAAC 18
 DB 17 CTGAGCAATACCTAGC 2
 RESULT 22
 US-08-482-182-6/0
 Sequence 6, Application US/08/08421182
 Patent No. 5861273
 GENERAL INFORMATION:
 APPLICANT: MACCARENAS, DESMOND
 APPLICANT: OLSON, PAMELA S.
 TITLE OF INVENTION: CHROMOSOMAL EXPRESSION OF HETEROLOGOUS
 TITLE OF INVENTION: GENES IN PATERNAL CHRIS
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRISON & FORSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

TOPOLOGY: linear
 ID: 207-772-41

Query Match: 48.1% Score 11, DB 1, Length 15,
 Best Local Similarity: 76.2%, Pred. No. 1.6e+03,
 Matches: 14, Conservative: 4, Mismatches: 1, Indels: 0,

QY 4 CTGAGTAACTAACTAAC 24
 ID 10 TTAGCATATATCTAAGAAGAA 10

RESULT 17

US-09-070-408-131/c
 Sequence: 131, Application US/09/070408
 Patent No. 6180441

GENERAL INFORMATION:

APPLICANT: Iqbal, Brent L.

APPLICANT: Iqbal, Brent L.

APPLICANT: Iqbal, Brent L.

APPLICANT: Iqbal, Brent L.

APPLICANT: Iqbal, Brent L.

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APPLICANT: Iqbal, Brent L.

APPLICANT: Iqbal, Brent L.

APPLICANT: Iqbal, Brent L.

APPLICANT: Iqbal, Brent L.

APPLICANT: Iqbal, Brent L.

APPLICANT: Lemmel, Steven A.
 APPLICANT: Leonard, Amanda Elin Young
 APPLICANT: Chaudhary, Sumita
 TITLE OF INVENTION: 3D/4D SCENES EXTRACTING CONTINUED
 FILE REFERENCE: 6004 US, P1
 CURRENT APPLICATION NUMBER: 09/04/011, 028A
 PRIOR FILING DATE: 1998-08-07
 PRIOR APPLICATION NUMBER: US 08/064,440
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 16
 LENGTH: 19
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Filter: F074
 US-09-131-028A-16

Query Match: 47.4% Score 12.8, DB 4, Length 19,
 Best Local Similarity: 87.5%, Pred. No. 1.6e+03,
 Matches: 14, Conservative: 9, Mismatches: 7, Indels: 0, Gaps: 0,

QY 3 CTGAGTAACTAACTAAC 18
 ID 16 CTGAGTAACTAACTAAC 1

RESULT 19

PCT-US96-05611A-18/c

Sequence: 18, Application PCT/US9605611A

GENERAL INFORMATION:

APPLICANT: Mueller, John P.

APPLICANT: Leonard, Michael J.

APPLICANT: McFarland, Henry F.

APPLICANT: Mats, Louis A.

APPLICANT: Mueller, Eileen Elliott

APPLICANT: Nye, Steven H.

APPLICANT: Felicity, Clara M.

APPLICANT: Squinto, Stephen P.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

APPLICANT: Wilkins, James A.

STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2466
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 144 KB
 MEDIUM TYPE: 5.25" Diskette
 OPERATING SYSTEM: IBM PC compatible
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 12/10/1994
 FILING DATE: January 11, 1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 680000074
 FILING DATE: October 26, 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Marburg, Richard J
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 218/064
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 490-1666
 TELEFAX: (213) 967-0448
 TELEX: 67-3510
 INFORMATION FOR SEQ IN NO: 0755
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 OTHER INFORMATION: The letter "m" represents the stop in region
 OTHER INFORMATION: of an mRNA library.
 US-09-894-040-6764
 Query Match: 48.1% Score 13, DB 4, Length 27,
 Desc Local Simulation: 68.0% Find No: 15035,
 Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, gaps: 0

CV 6 AGCAAGCTTCAAGCAAGCAATA 27
 ||||| ||||| ||||| |||||
 DB 1 AGCAAGCTTCAAGCAAGCAATA 27

RESULT 15
 US-09-475-063-41/C
 Sequence ID: 4411001100-0010047503
 Patent No: 575013
 GENERAL INFORMATION:
 APPLICANT: Paolelli, Enzo
 APPLICANT: Taylor, Jill
 APPLICANT: Antaglia, James
 APPLICANT: Ross, Louis
 TITLE OF INVENTION: Malaria Disease Virus Recombinant
 TITLE OF INVENTION: Foxvirus Vaccine
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 ADDRESS: 530 Fifth Avenue
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PASCAL FORMAL-#1.0, Visual #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 05/08/475,063
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 00/03/207,792
 FILING DATE: 04-JAN-1993
 APPLICATION NUMBER: US 08/001,391
 FILING DATE: 04-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 APPLICATION NUMBER: 55,576
 REFERENCE/DOCKET NUMBER: 454310-2480
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 940-3333
 TELEFAX: (212) 940-3333
 INFORMATION FOR SEQ IN NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-475-063-41
 Query Match: 45.1% Score 13, DB 1, Length 45,
 Desc Local Simulation: 66.0% Find No: 15607,
 Matches: 16, Conservative: 0, Mismatches: 5, Indels: 0, gaps: 0

CV 4 TGGGATATCTGTAAGAGAA 24
 ||||| ||||| ||||| |||||
 DB 30 TGGGATATCTGTAAGAGAA 10

RESULT 16
 US-08-207-792-41/C
 Sequence ID: Application ID: 00000002
 Patent No: 55556
 GENERAL INFORMATION:
 APPLICANT: Paolelli, Enzo
 APPLICANT: Taylor, Jill
 APPLICANT: Antaglia, James
 APPLICANT: Ross, Louis
 TITLE OF INVENTION: Malaria Disease Virus Recombinant
 TITLE OF INVENTION: Foxvirus Vaccine
 NUMBER OF SEQUENCES: 45
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtis, Morris & Safford
 ADDRESS: 530 Fifth Avenue
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: New York
 COUNTRY: United States of America
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PASCAL FORMAL-#1.0, Visual #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 01/05/792,792
 FILING DATE:
 CLASSIFICATION: 425
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 00/06/301,391
 FILING DATE: 04-JAN-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2480
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 940-3333
 TELEFAX: (212) 940-3333
 INFORMATION FOR SEQ IN NO: 41:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 45 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

Matches 18, Conservative 0, Mismatches 8, Totals 0, Gaps 0

QY 2 CCGAGCAATACCTACCAATA 27
 ||||| ||||| ||||| |||||
 TB 2 CCGAGCAATACCTACCAATA 27

RESULT 11
 US 08 896-176 7
 ? Sequence 3, Application US/0804176
 ? Patent No. 5985581
 ? GENERAL INFORMATION:
 ? APPLICANT: Nixon, Ralph A.
 ? APPLICANT: Cataldo, Anne M.
 ? APPLICANT: Kay, Benjamin B.
 ? APPLICANT: Mathews, Paul M.
 ? TITLE OF INVENTION: USE OF PRESENTIN 1 FOR DIAGNOSIS OF
 ? FILE REFERENCE: 0441/028002
 ? CURRENT APPLICATION NUMBER: 28/ 4760,176
 ? CURRENT FILING DATE: 1997-07-17
 ? EARLIER APPLICATION NUMBER: 65/022,594
 ? EARLIER FILING DATE: 1996-07-25
 ? NUMBER OF SEQ ID NOS: 10
 ? SOFTWARE: FASTSEQ for Windows Version 3.0
 ? SEQ ID NO: 7
 ? LENGTH: 28
 ? TYPE: DNA
 ? ORGANISM: Homo sapiens
 US 08 896-176 7

Query Match 48.94, Score 13.2, DP 3, Length 28
 Best Local Similarity 83.38, Field No. 1,26+03
 Matches 19, Conservative 0, Mismatches 1, Totals 0, Gaps 0

QY 2 CCGAGCAATACCTACCAATA 19
 ||||| ||||| ||||| |||||
 TB 11 CCGAGCAATACCTACCAATA 28

RESULT 12
 US 09-251-565 11
 ? Sequence 11, Application US/09251565
 ? Patent No. 6130073
 ? GENERAL INFORMATION:
 ? APPLICANT: Payco, Patricia F. et al, Applied Pl. Systems Division
 ? TITLE OF INVENTION: Combed Amplification and Ligation Method
 ? NUMBER OF SEQUENCES: 75
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESS: David J. Woltz, Wilson-Sundin-Goodrich & Fosatti
 ? STREET: 670 Elm Mill Road
 ? CITY: Palo Alto
 ? STATE: California
 ? COUNTRY: USA
 ? ZIP: 94304-1050
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5 inch diskette
 ? COMPUTER: IBM compatible
 ? OPERATING SYSTEM: Microsoft Windows 98/MS 5.0
 ? SOFTWARE: MacEdit-1.0 for Windows 9.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: 09/075,932
 ? FILING DATE: 09/07/2000
 ? CLASSIFICATION:
 ? PRIORITY APPLICATION DATA:
 ? APPLICATION NUMBER: 09/075,932
 ? FILING DATE: 09/07/99
 ? PRIORITY APPLICATION DATA:
 ? APPLICATION NUMBER: 08/090,496
 ? FILING DATE: 13-AUG-94
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: David J. Woltz

REGISTRATION NUMBER: 18,162
 REFERENCE/DOCKET NUMBER: 16442-754
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 493-9300
 TELEFAX: (650) 493-6811
 INFORMATION FOR SEQ. ID NO: 11:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 28 nucleotides
 ? TYPE: nucleic acid
 ? STRANES: single
 ? TOPOLOGY: linear
 US 09-251-565-11

Query Match 48.94, Score 13.2, DP 3, Length 28
 Best Local Similarity 69.28, Field No. 1,26+03
 Matches 18, Conservative 0, Mismatches 8, Totals 0, Gaps 0

QY 2 CCGAGCAATACCTACCAATA 27
 ||||| ||||| ||||| |||||
 TB 2 CCGAGCAATACCTACCAATA 27

RESULT 13
 US-09-081-576-9
 ? Sequence 3, Application US/09081576A
 ? Patent No. 6180111
 ? GENERAL INFORMATION:
 ? APPLICANT: Stein, Daniel C.
 ? TITLE OF INVENTION: VASTAR DELIVERY SYSTEM
 ? FILE REFERENCE: 2747 0097 27 CIP (8014-014)
 ? CURRENT APPLICATION NUMBER: US/09/081,576A
 ? CURRENT FILING DATE: 1998-06-19
 ? PRIOR APPLICATION NUMBER: US 08/236,422
 ? PRIOR FILING DATE: 1997-03-23
 ? PRIOR APPLICATION NUMBER: US 08/443,514
 ? PRIOR FILING DATE: 1995-05-18
 ? NUMBER OF SEQ ID NOS: 13
 ? SOFTWARE: PatentIn Ver. 2.0
 ? SEQ ID NO: 9
 ? LENGTH: 35
 ? TYPE: DNA
 ? ORGANISM: Neisseria gonorrhoeae
 US-09-081-576-9

Query Match 48.94, Score 13.2, DP 4, Length 35
 Best Local Similarity 81.38, Field No. 1,36+03
 Matches 19, Conservative 0, Mismatches 1, Totals 0, Gaps 0

QY 3 AATATACCAATACCAAT 26
 ||||| ||||| ||||| |||||
 TB 12 AATATACCAATACCAAT 29

RESULT 14
 US-08-540-675-6
 ? Sequence 6756, Application US/08540675
 ? Patent No. 6346398
 ? GENERAL INFORMATION:
 ? APPLICANT: Payco, Pamela
 ? APPLICANT: McSwigen, James
 ? APPLICANT: Stinchcomb, Dan T.
 ? APPLICANT: Escobedo, Jaime
 ? TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 ? TITLE OF INVENTION: TREATMENT OF DISEASES OR
 ? TITLE OF INVENTION: CONDITIONS RELATED TO LEVELS
 ? TITLE OF INVENTION: OF VASULAR ENDOTHELIAL
 ? TITLE OF INVENTION: GROWTH FACTOR
 ? NUMBER OF SEQUENCES: 402
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESS: Lynn S. Lynn
 ? STREET: 633 West Fifth Street
 ? CITY: Los Angeles

```

      ATTENTION:
      NAME: Marburg, Richard J.
      FLUORESCENT NUMBER: 21,027
      REFERENCE NUMBER: 21,004
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 493-1900
      TELEFAX: (415) 955-0440
      TELETYPE: 67-3810
      INFORMATION FOR SEQ ID NO: 3413:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 27 base pairs
      TYPE: nucleic acid
      STRATEGY: single
      TOPOLOGY: linear
      FEATURE:
      CDS: INTERVIEW: The letter 'T' represents the start of region
      with information of the 1st type.
      US-98-094 940 4413

Query Match      48.3%  Score 13.27  DB 2  Length 173
      Dact local similarity 63.0%  Pred. No. 1.2e+03
      Matches 12; Conservative 3; Mismatches 4; Indels 1; Gaps 0

Cg      8  CCAATCTACGACAAAT 26
      |||:::|||||
      3  CAAATCGGAGGAGGAAAT 21

Result 10
US-98-353-922 11
      Reference 11; Identification 97.9997902
      Patent No. 5912148
      GENERAL INFORMATION:
      APPLICANT: Perkin Elmer Corporation, Applied Biosystems Division
      TITLE OF INVENTION: Coupled Amplification and Digestion Method
      NUMBER OF SEQUENCES: 75
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: David J. Weitz, Wilson Consulting Goodrich & Rosati
      STREET: 650 Page Mill Road
      City: Palo Alto
      STATE: California
      COUNTRY: USA
      ZIP: 94304-1050
      COMPUTER READABLE FORM:
      MEDIUM TYPE: 3.5 inch diskette
      COMPUFLEX: IBM compatible
      OPERATING SYSTEM: Macintosh Windows version 5.0
      SOFTWARE: Windows for window 6.0,
      DELIMITER: ASCII, fixed text format
      CURRENT AFFILIATION DATA:
      AFFILIATION NUMBER: US-98-353-922
      FILING DATE:
      CLASSIFICATION:
      PRIOR AFFILIATION DATA:
      APPLICATION NUMBER: 09/792,696
      FILING DATE: 19-AUG-94
      ATTORNEY/AGENT INFORMATION:
      NAME: David J. Weitz
      REGISTRATION NUMBER: 39,362
      REFERENCE/WORKER NUMBER: PERM4215
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (415) 493-9300
      TELEFAX: (415) 493-6811
      INFORMATION FOR SEQ ID NO: 13:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 28 nucleotides
      TYPE: nucleic acid
      STRATEGY: single
      TOPOLOGY: linear
      US-98-094 945 902 11

Query Match      48.9%  Score 13.27  DB 2  Length 173
      Dact local similarity 63.0%  Pred. No. 1.2e+03
      Matches 12; Conservative 3; Mismatches 4; Indels 1; Gaps 0

```

SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRAINDNESS: single
 TOPOLOGY: linear

US-09-439-628-02

Query Match 49.94, Score 13.6, DB 2, Length 31,
 Best Local Similarity 90.00, Field No. 8-49-02,
 Matches 17, Conservative 0, Mismatches 4, Indels 0, Gaps 0.

QY 2 CTATACATACCAACAA 21
 DB 22 CTATACATACCAACAA 3

RESULT 6

US-07-662-7640-14
 Sequence 14, Application us/076627640

Patent No. 5966183

GENERAL INFORMATION:

APPLICANT: FISHBELL, GEORGE
 TITLE OF INVENTION: METHOD AND MEANS FOR SETTING AND
 TITLE OF INVENTION: IDENTIFYING MOLECULAR INFORMATION

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: LERBER, DAVID, LITTEBERG, RONALD &

ADDRESS: MENTHILL

STREET: 600 South, Avenue West

CITY: Westfield

STATE: New Jersey

COUNTRY: USA

ZIP: 07090

COMPUTER PREPARABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC COMPATIBLE

SOFTWARE: P4-00 In Release #1.0, Version #1.10

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/662,7640

FILING DATE: 28 FEB 1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/201,358

FILING DATE: 26 MAY-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 62/770,346

FILING DATE: 28 AUG 1985

ATTORNEY/AGENT INFORMATION:

NAME: Foley, Shawn P.

REGISTRATION NUMBER: 33,071

REFERENCE/AGENT NUMBER: 13E-3H/0002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 908-654-5000

TELEFAX: 908-654-7866

INFORMATION FOR SEQ ID NO. 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 21 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-07-662,7640-14

Query Match 49.94, Score 13.6, DB 2, Length 21,
 Best Local Similarity 90.00, Field No. 8-49-02,
 Matches 17, Conservative 0, Mismatches 4, Indels 0, Gaps 0.

QY 8 CTATACATACCAACAA 25
 DB 4 CTATACATACCAACAA 21

RESULT 7

US-09-766-439-67
 Sequence 67, Application us/09766439

Patent No. 592538

GENERAL INFORMATION:

APPLICANT: HAZEL, JAMES WILLIAM

APPLICANT: JENSEN, MARK ANTON

TITLE OF INVENTION: GENETIC MARKERS ANT METHYLO

TITLE OF INVENTION: THE DETECTION OF LISTERIA

TITLE OF INVENTION: W3 VIRUS AND LISTERIA SPT.

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: U.S.A.

ZIP: 19898

J. METTER HEVACHE FORM

MEDIUM TYPE: 1.50 INCH DISKETTE

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: MICROSOFT WINDOWS 3.1

SOFTWARE: MICROSOFT WORD 6.00

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/766,439

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/45,228

FILING DATE: NOVEMBER 8, 1996

ATTORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AYAMETHY

REGISTRATION NUMBER: 23,692

REFERENCE/DOCKET NUMBER: MD-1065-A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 302-773-0164

INFORMATION FOR SEQ ID NO. 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 26 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-09-766-439-67

Query Match 49.94, Score 13.6, DB 2, Length 26,
 Best Local Similarity 83.33, Field No. 1-29-03,
 Matches 15, Conservative 0, Mismatches 3, Indels 0, Gaps 0.

QY 9 AATACCTAACCAACAAI 26
 DB 2 AATACCTAACCAACAAI 19

RESULT 8

US-08-766-439-68
 Sequence 68, Application us/08766439

Patent No. 592538

GENERAL INFORMATION:

APPLICANT: HAZEL, JAMES WILLIAM

APPLICANT: JENSEN, MARK ANTON

TITLE OF INVENTION: GENETIC MARKERS AND METHODS FOR

TITLE OF INVENTION: THE DETECTION OF LISTERIA

TITLE OF INVENTION: W3 VIRUS AND LISTERIA SPT.

NUMBER OF SEQUENCES: 110

CORRESPONDENCE ADDRESS:

ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY

STREET: 1007 MARKET STREET

CITY: WILMINGTON

STATE: DELAWARE

COUNTRY: U.S.A.

ZIP: 19898

```

07      6 ACATACCTGTAAGCGAACAATT 26
          |||||:|||||
08      1 AATATAATGTTCATGAAGAATAAT 21

```

REFERENCE/INVENT NUMBER: 07025
TELEPHONE/MAILING INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67 3510
INFORMATION FOR SEQ ID NO.: 22
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

GC 28.3% GC/AT 22

Query Match Score 13.6; DB 1; Length 33;
Best local similarity at pos. 1; First Mb 8.4e+02;
Matching 15; Threshold 1; Max. G/Ces 4; Index 2; Type

07 2 CCGACGCAAAAGCCATCAA 31
||||| ||||
22 CCGACGCAAAAGCCATCAA 3

RESULT 5
CDS: 131-136 nt
Sequence No. Application No./Accession No.
Patent No. 5817796

GENERAL INFORMATION:
APPLICANT: Stinchcomb, Dan T.
APPLICANT: Draper, Kenneth
APPLICANT: McGwigen, James
APPLICANT: Jarvis, Thale
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
TREATMENT OF EPITHELIOID AND
TITLE OF INVENTION: CANCER USING RETROVIRUS
NUMBER OF SEQUENCES: 2127
CORRESPONDENCE ADDRESS:
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COUNTRY: U.S.A.
ZIP: 90071

CURRENT AVAILABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C., DOS 5.0
E-MAIL: worldnet@att.net

CURRENT APPLICATION DATA: J05 5.0
APPLICATION NUMBER: 55793-415-628
FILING DATE: 05-MAY-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 1917744
FILING DATE: January 13, 1995
APPLICATION NUMBER: 57-41,466
FILING DATE: May 18, 1994
APPLICATION NUMBER: 06742,943
FILING DATE: February 7, 1994
APPLICATION NUMBER: 07487,132
FILING DATE: December 7, 1992
APPLICATION NUMBER: 07356,122
FILING DATE: August 26, 1992

ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard
REGISTRATION NUMBER: 27,427
REFERENCE/INVENT NUMBER: 07025
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION 5-4-95 10:11 AM 42;

685	10.2	17.7	15	US-08-624-895-11	Sequence 11, Appl	758	10	17.0	23	1	US-08-656-716-40	Sequence 43, Appl
686	10.2	17.8	35	US-08-650-961-17	Sequence 17, Appl	759	10	17.0	23	1	US-08-657-76-F-63	Sequence 44, Appl
687	10.2	17.8	35	US-08-771-466-10	Sequence 10, Appl	760	10	17.0	23	1	US-08-657-115-3	Sequence 16, Appl
688	10.2	17.8	14	US-08-645-494-64	Sequence 63, Appl	761	10	17.0	23	1	US-08-658-929-16	Sequence 17, Appl
689	10	17.0	14	US-08-753-147-132	Sequence 132, Appl	762	10	17.0	23	1	US-08-658-929-16	Sequence 18, Appl
690	10	17.0	17	US-08-650-740-21	Sequence 21, Appl	763	10	17.0	23	1	US-08-658-929-16	Sequence 19, Appl
691	10	17.0	17	US-08-650-740-21	Sequence 21, Appl	764	10	17.0	23	1	US-08-658-929-16	Sequence 20, Appl
692	10	17.0	17	US-08-650-740-21	Sequence 21, Appl	765	10	17.0	23	1	US-08-658-929-16	Sequence 21, Appl
693	10	17.0	17	US-08-650-740-21	Sequence 21, Appl	766	10	17.0	23	1	US-08-658-929-16	Sequence 22, Appl
694	10	17.0	18	US-08-448-580-17	Sequence 17, Appl	767	10	17.0	23	1	US-08-658-929-16	Sequence 23, Appl
695	10	17.0	18	US-08-448-580-17	Sequence 17, Appl	768	10	17.0	23	1	US-08-658-929-16	Sequence 24, Appl
696	10	17.0	18	US-08-643-212-39	Sequence 19, Appl	769	10	17.0	23	1	US-08-658-929-16	Sequence 25, Appl
697	10	17.0	18	US-08-941-155-13	Sequence 13, Appl	770	10	17.0	23	1	US-08-658-929-16	Sequence 26, Appl
698	10	17.0	18	US-08-612-580A-85	Sequence 85, Appl	771	10	17.0	23	1	US-08-658-929-16	Sequence 27, Appl
699	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	772	10	17.0	23	1	US-08-658-929-16	Sequence 28, Appl
700	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	773	10	17.0	23	1	US-08-658-929-16	Sequence 29, Appl
701	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	774	10	17.0	23	1	US-08-658-929-16	Sequence 30, Appl
702	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	775	10	17.0	23	1	US-08-658-929-16	Sequence 31, Appl
703	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	776	10	17.0	23	1	US-08-658-929-16	Sequence 32, Appl
704	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	777	10	17.0	23	1	US-08-658-929-16	Sequence 33, Appl
705	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	778	10	17.0	23	1	US-08-658-929-16	Sequence 34, Appl
706	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	779	10	17.0	23	1	US-08-658-929-16	Sequence 35, Appl
707	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	780	10	17.0	23	1	US-08-658-929-16	Sequence 36, Appl
708	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	781	10	17.0	23	1	US-08-658-929-16	Sequence 37, Appl
709	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	782	10	17.0	23	1	US-08-658-929-16	Sequence 38, Appl
710	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	783	10	17.0	23	1	US-08-658-929-16	Sequence 39, Appl
711	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	784	10	17.0	23	1	US-08-658-929-16	Sequence 40, Appl
712	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	785	10	17.0	23	1	US-08-658-929-16	Sequence 41, Appl
713	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	786	10	17.0	23	1	US-08-658-929-16	Sequence 42, Appl
714	10	17.0	18	US-08-444-604-13	Sequence 13, Appl	787	10	17.0	23	1	US-08-658-929-16	Sequence 43, Appl
715	10	17.0	18	US-08-444-604-13	Sequence 13, Appl							

393	10.4	37.3	30	4	US-08-408-444A-4	Sequence 8, Appl
394	10.6	37.3	31	3	US-08-408-444B-4	Sequence 22, Appl
395	10.6	37.3	32	3	US-08-408-444C-4	Sequence 2, Appl
396	10.6	37.3	33	3	US-08-408-444D-4	Sequence 2, Appl
397	10.6	37.3	34	3	US-08-408-444E-4	Sequence 33, Appl
398	10.6	37.3	35	3	US-08-408-444F-4	Sequence 23, Appl
399	10.6	37.3	36	3	US-08-408-444G-4	Sequence 13, Appl
400	10.6	37.3	37	3	US-08-408-444H-4	Sequence 46, Appl
401	10.6	37.3	38	3	US-08-408-444I-4	Sequence 33, Appl
402	10.6	37.3	39	3	US-08-408-444J-4	Sequence 21, Appl
403	10.6	37.3	40	3	US-08-408-444K-4	Sequence 11, Appl
404	10.6	37.3	41	3	US-08-408-444L-4	Sequence 21, Appl
405	10.6	37.3	42	3	US-08-408-444M-4	Sequence 11, Appl
406	10.6	37.3	43	3	US-08-408-444N-4	Sequence 21, Appl
407	10.6	37.3	44	3	US-08-408-444O-4	Sequence 27, Appl
408	10.6	37.3	45	3	US-08-408-444P-4	Sequence 27, Appl
409	10.6	37.3	46	3	US-08-408-444Q-4	Sequence 27, Appl
410	10.6	37.3	47	3	US-08-408-444R-4	Sequence 41, Appl
411	10.6	37.3	48	3	US-08-408-444S-4	Sequence 41, Appl
412	10.6	37.3	49	3	US-08-408-444T-4	Sequence 41, Appl
413	10.6	37.3	50	3	US-08-408-444U-4	Sequence 41, Appl
414	10.6	37.3	51	3	US-08-408-444V-4	Sequence 41, Appl
415	10.6	37.3	52	3	US-08-408-444W-4	Sequence 41, Appl
416	10.6	37.3	53	3	US-08-408-444X-4	Sequence 41, Appl
417	10.6	37.3	54	3	US-08-408-444Y-4	Sequence 41, Appl
418	10.6	37.3	55	3	US-08-408-444Z-4	Sequence 41, Appl
419	10.6	37.3	56	3	US-08-408-444AA-4	Sequence 41, Appl
420	10.6	37.3	57	3	US-08-408-444AB-4	Sequence 41, Appl
421	10.6	37.3	58	3	US-08-408-444AC-4	Sequence 41, Appl
422	10.4	37.3	59	3	US-08-408-444AD-4	Sequence 41, Appl
423	10.4	37.3	60	3	US-08-408-444AE-4	Sequence 41, Appl
424	10.4	37.3	61	3	US-08-408-444AF-4	Sequence 41, Appl
425	10.4	37.3	62	3	US-08-408-444AG-4	Sequence 41, Appl
426	10.4	37.3	63	3	US-08-408-444AH-4	Sequence 41, Appl
427	10.4	37.3	64	3	US-08-408-444AI-4	Sequence 41, Appl
428	10.4	37.3	65	3	US-08-408-444AJ-4	Sequence 41, Appl
429	10.4	37.3	66	3	US-08-408-444AK-4	Sequence 41, Appl
430	10.4	37.3	67	3	US-08-408-444AL-4	Sequence 41, Appl
431	10.4	37.3	68	3	US-08-408-444AM-4	Sequence 41, Appl
432	10.4	37.3	69	3	US-08-408-444AN-4	Sequence 41, Appl
433	10.4	37.3	70	3	US-08-408-444AO-4	Sequence 41, Appl
434	10.4	37.3	71	3	US-08-408-444AP-4	Sequence 41, Appl
435	10.4	37.3	72	3	US-08-408-444AQ-4	Sequence 41, Appl
436	10.4	37.3	73	3	US-08-408-444AR-4	Sequence 41, Appl
437	10.4	37.3	74	3	US-08-408-444AS-4	Sequence 41, Appl
438	10.4	37.3	75	3	US-08-408-444AT-4	Sequence 41, Appl
439	10.4	37.3	76	3	US-08-408-444AU-4	Sequence 41, Appl
440	10.4	37.3	77	3	US-08-408-444AV-4	Sequence 41, Appl
441	10.4	37.3	78	3	US-08-408-444AW-4	Sequence 41, Appl
442	10.4	37.3	79	3	US-08-408-444AX-4	Sequence 41, Appl
443	10.4	37.3	80	3	US-08-408-444AY-4	Sequence 41, Appl
444	10.4	37.3	81	3	US-08-408-444AZ-4	Sequence 41, Appl
445	10.4	37.3	82	3	US-08-408-444BA-4	Sequence 41, Appl
446	10.4	37.3	83	3	US-08-408-444BB-4	Sequence 41, Appl
447	10.4	37.3	84	3	US-08-408-444BC-4	Sequence 41, Appl
448	10.4	37.3	85	3	US-08-408-444BD-4	Sequence 41, Appl
449	10.4	37.3	86	3	US-08-408-444BE-4	Sequence 41, Appl
450	10.4	37.3	87	3	US-08-408-444BF-4	Sequence 41, Appl
451	10.4	37.3	88	3	US-08-408-444BG-4	Sequence 41, Appl
452	10.4	37.3	89	3	US-08-408-444BH-4	Sequence 41, Appl
453	10.4	37.3	90	3	US-08-408-444BI-4	Sequence 41, Appl
454	10.4	37.3	91	3	US-08-408-444BJ-4	Sequence 41, Appl
455	10.4	37.3	92	3	US-08-408-444BK-4	Sequence 41, Appl
456	10.4	37.3	93	3	US-08-408-444BL-4	Sequence 41, Appl
457	10.4	37.3	94	3	US-08-408-444BM-4	Sequence 41, Appl
458	10.4	37.3	95	3	US-08-408-444BN-4	Sequence 41, Appl
459	10.4	37.3	96	3	US-08-408-444BO-4	Sequence 41, Appl
460	10.4	37.3	97	3	US-08-408-444BP-4	Sequence 41, Appl
461	10.4	37.3	98	3	US-08-408-444BQ-4	Sequence 41, Appl
462	10.4	37.3	99	3	US-08-408-444BR-4	Sequence 41, Appl
463	10.4	37.3	100	3	US-08-408-444BS-4	Sequence 41, Appl
464	10.4	37.3	101	3	US-08-408-444BT-4	Sequence 41, Appl
465	10.4	37.3	102	3	US-08-408-444BU-4	Sequence 41, Appl

[illegible]

2. via p75^{NTR} maturation. The TrkA192 subdomain comprises a portion of the extracellular domain of TrkA. The Ig-like subdomain 2 is the portion of TrkA responsible for binding neurotrophins such as nerve growth factor (NGF). TrkA192 binds NGF with high affinity, inhibiting its biological activity in vitro and in vivo. NGF is one of a family of neurotrophins involved in the development and maintenance of the peripheral and central nervous system, being a potent neurotrophic factor for maintain cholinergic neurons and promoting the survival and differentiation of sympathetic and sensory neurons during development. NGF also acts as a mediator of some persistent pain states by interacting with TrkA in DRG is of a sub-group of the TrkA192. Sensory neurons of the dorsal root ganglion. The action of NGF on TrkA receptors causes an increase in neuropeptide levels in these sensory neurons and affects sodium and calcium channels such that these neurons are increased in excitability. In chronic inflammatory states (e.g., arthritis, Ruyter cystitis), the effects of constantly elevated NGF levels result in a long-term disabling pain state. NGF upregulation is also likely to be involved in post-herpetic neuralgia which is associated with shingles. TrkA-derived peptides which bind NGF can be used to reduce NGF levels and thus to treat pain associated with NGF (or other neurotrophin) upregulation e.g., pain symptomatic of idiopathic sensory urgency, interstitial cystitis, arthritis, shingles, peripheral inflammation, chronic inflammation or postherpetic neuralgia. They may be used to screen for molecules that bind to TrkA, to identify molecules that enhance binding to a neurotrophin, to identify neurotrophin analogues, and may be administered therapeutically to treat patients with Alzheimer's disease. TrkA peptides and nucleotides are also useful as diagnostic probes.

Sequence 19 B17: 1 A; 4 C; 6 G; 6 T; 0 other;

Query Match: 47.4%; Score 12.9; DB 21; Length 19;
 Best Local Similarity: 87.58; Pred. NO: 1.6e+04;
 Matches: 14; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0;

QY 3 CTGACGCAATACCTAAC 18
 |||||
 DB 16 CTGACGCAATACCTAAC 1

Search completed: July 21, 2003, 14:06:05
 Job time: 108.101 secs

CS Synthesis.
 XX WO2000034465-A2.
 XX
 PD 15-JUN 2000.
 XX
 XX 11-DEC-1999; 99WO-00A0102
 XX
 XX 08-DEC-1999; 99US-0297389.
 XX
 XX 0399P: EFFECTIVENESS OF THE BETA-CASEIN GENE
 XX
 XX Mastomys 2;
 XX
 DR WPI; 2000-422415/26.
 XX
 PT Isolated nucleic acid molecule for obtaining human beta-casein in animal
 PT encodes Nucleotide sequence for beta-casein protein in Aspidoptera
 PT Immunoglobulin Hsp60 and Gamma globulin Hsp60 polypeptide
 XX
 XX Example 7; Page 62, 118FF, English.
 XX
 SC The Hsp60 heat shock protein or fragment derived from a host cell
 CC means of the host cell and the Hsp60 heat shock protein is a fragment of the
 CC from Aspidoptera Immunoglobulin Hsp60 and Gamma globulin can be used as
 CC Immunoglobulin to give protective immunity from these microorganisms.
 CC Nucleotide sequences encoding these proteins are useful for
 CC producing recombinant proteins for immunizing an animal or as
 CC probes and/or primers to detect the microorganisms in a biological
 CC sample.
 XX
 SC Sequence 19 BP, 3 A, 4 C, 6 G, 6 T, 0 other;
 XX
 CY Query Match 1748, 1749, 1750, 1751, Length 19;
 DB Best Local Similarity 97.63, Posit. No. 160104;
 Matches 14, Conservation 0, Mismatched 2, Indels 0, Gaps 0;
 XX
 CY 3 CTGAGCAATACCTTAC 18
 DB 16 CTGAGCAATACCTTAC 1
 XX
 RESULT 19
 AA250913/c
 ID AA250913 standard, DNA, 19 BP.
 XX
 AC AA250913;
 XX
 CT 31-MAY-2000 (first entry)
 XX
 DE PCR primer R074 to amplify human beta-casein gene.
 XX
 KW Plasmid PRAB-84-69; recombinant beta-casein human PCR primer;
 KW casein kinase II alpha subunit; casein kinase II beta subunit;
 KW karyotype resistance marker; immunoglobulin; protein stability;
 KW pharmaceutical; nutritional composition; vaccine formulation; CO.
 XX
 OS Homo sapiens.
 XX
 PN WO200008174-A1.
 XX
 PD 17-FEB 2000.
 XX
 PF 06-AUG-1999; 99WO-US17873.
 XX
 PF 07-AUG 1999; 99US-0141028.
 XX
 PA ABBO (ABBO) LAB.
 XX
 PI Mukerji P, Lemmel SA, Leonard AE, Chaudhary S;
 XX
 XX WPI; 2000-257731/19

PT Resultant construct useful for producing human milk protein, either
 PT plant protein, antibody, antigen or hormone, comprises nucleotide
 PT sequences expressing beta-casein protein.
 XX
 XX Example 1; Page 11; 73pp; English.
 XX
 SC The patent discloses a method of producing human milk protein, either
 CC plant protein, antibody, antigen or hormone, comprising nucleotide
 CC transforming host cells with a vector comprising the gene
 CC of interest linked to a promoter and nucleotide sequences encoding
 CC subunit of a kinase, protein kinase and a peptidase, has proved to be
 CC useful for improving the genetic stability of a plasmid containing
 CC pharmaceutical or nutritional compositions and in vaccine formulations.
 CC The present sequence is that of PCR primer R074, used to amplify human
 CC beta-casein gene for construction of plasmid PRAB-84-69; PRAB-84-69
 CC contains a plasmid gene encoding human beta-casein, human kinase II
 CC alpha and beta subunit, bacterial resistance marker and
 CC immunoprecipitation.
 XX
 SC Sequence 19 BP, 3 A, 4 C, 6 G, 6 T, 0 other;
 XX
 CY Query Match 1748, 1749, 1750, 1751, Length 19;
 DB Best Local Similarity 97.63, Posit. No. 160104;
 Matches 14, Conservation 0, Mismatched 2, Indels 0, Gaps 0;
 XX
 CY 3 CTGAGCAATACCTTAC 18
 DB 16 CTGAGCAATACCTTAC 1
 XX
 RESULT 40
 AA250208/c
 ID AA250208 standard, DNA, 19 BP.
 XX
 AC AA250208;
 XX
 CT 15-FEB-2000 (first entry)
 XX
 DE T7 terminator PCR primer.
 XX
 KW Tyrosine kinase, TykA, immunoglobulin, Ig, adhesion binding;
 KW neurotrophin, nerve growth factor, NGF, inhibition, pain, sensory;
 KW synaptophysin, neuron, TykA receptor; nonreceptor, dorsal foot ganglion;
 KW chronic inflammatory states; upregulation; treatment; arthritis;
 KW inflammatory sensory system; inflammatory system; standard;
 KW inflammation; postherpetic neuralgia; analgesic; Alzheimer's disease;
 KW diagnosis; splice variant; PCR; primer; ss.
 XX
 OS Synthetic.
 OS Bacteriophage T7.
 XX
 PN WO9903005-A2.
 XX
 PD 21-JUN 1999.
 XX
 PF 09-APR 1999; 99WO-CR01108.
 XX
 PF 09-APR 1999; 99GB-0007781.
 XX
 PA (UYER-) UNIV BRISTOL.
 XX
 PI Robertson AGS, Allen SJ, Dabkarn D;
 XX
 DR WPI; 2000-023041/02.
 XX
 PF Novel plasmid vector useful for treating Alzheimer's disease antigen in
 PT e.g. arthritis, shingles etc.
 XX
 XX Example 2; Page 14; 67pp; English.
 CC PCR primers AA23025 and 23026 were used to create a cDNA encoding a portion
 CC of human tyrosine kinase TykA immunoglobulin. The cDNA and protein

Query Match 48.1% Score 137 DB 14; Length 35;
Best Local Similarity 76.2% Pred. No. 1,46,04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4 TAAATATATCTAAAGAA 24
|||||
10 TAAATATATCTAAAGAA 10

RESULT 36

AAV26876/c
10 AAV26876 standard; DNA; 35 BP.

AAV26876;

01-SEP-1998 (first entry)

Record found for virus primer RM388.

01-SEP-1998; Matched disease virus; MVA; Jynthon; vaccination;
ss; PCR; primer; amplification.

Synthetic;

US759553 A.

02-JUN-1998.

07-JUN-1998; Gene 747667

07-MAR-1994; 94US-0207792.

07-MAR-1994; 94US-0666065.

11-JUN-1991; 91US-0713667.

13-JAN-1992; 92US-0840077.

06-MAR-1992; 92US-0847931.

04-JAN-1993; 93US-0001393.

12-AUG-1993; 94US-0105481.

07-JUN-1993; 90US-0476653.

(VIBO) VIRUSENERGIC CENTER.

Project F. Ross L. Tarraglia G. Taylor D.

WPI; 1998 11256/25.

Record found for virus containing Marek's disease virus DNA

for DNA vaccination of chickens (F. Tarraglia G. Taylor D.

glycoprotein

Example: 1; Column 19; 32pp; English.

The primers AAV26876/c were used in the production of a recombinant

vaccine virus containing exogenous DNA encoding Marek's disease virus

(MDV) gp and/or gp glycoprotein. The virus is useful for protecting

chickens against MDV infection by DNA vaccination, or for producing

recombinant MDV gp and/or gp glycoproteins.

Sequence 35 BP; 11 A; 7 C; 3 G; 14 T; 0 other;

Query Match 48.1% Score 137 DB 14; Length 35;
Best Local Similarity 76.2% Pred. No. 1,46,04;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

4 TAAATATATCTAAAGAA 24
|||||
10 TAAATATATCTAAAGAA 10

RESULT 37
AA742788/c
10 AA742788 standard; DNA; 19 BP.
XX

AA742788;

01-FEB-1997 (first entry)

T7 terminator primer.

Myelin basic protein; MBP; proteolipid protein; PLP;

multiple sclerosis; autoimmune disease; diagnosis; therapy;

T-lymphocyte; T-cell; apoptosis; primer; PCR;

polymerase chain reaction; ss.

Synthetic;

W09634622-A1.

07-NOV-1996.

22-APR-1996; 96WO-0505611.

07-JUN-1995; 95US-0482114.

12-MAY-1995; 95US-0416441.

02-MAY-1995; 95US-0431648.

(ALEX-) ALEXION PHARM INC.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Lenardo MJ, Matis L, McFarland HF, Mueller EE, Mueller JF,

Nye SH, Fellrey CM, Quinto OF, Wilkins JA,

WFI; 1996-05056/50.

New human myelin basic protein and proteolipid protein variant

used in the assessment, diagnosis and treatment of multiple

sclerosis

Example; Page 99; 156pp; English.

A PCR fragment that includes the human myelin basic protein (MBP)

exon 2 sequence was generated from pET22b/MBP78.5. See also

AA742785-86) using the sense oligonucleotide given in AA742787 in

combination with an antisense primer (AA742790) that hybridizes to

the T7 termination of pET22b. A second PCR fragment was generated

from the same template with a T7 promoter primer (AA742789) and an

antisense primer (AA742790) that hybridized to the 5' end of exon

2. Fusion of the PCR products by amplification with T7 promoter

and terminator primers completed the construction of a PCR

product containing the MBP-Xy39p1 gene (see also AA742789).

Sequence 19 BP; 4 A; 4 C; 6 G; 6 T; 0 other;

Query Match 47.4% Score 12.8; DB 17; Length 19;
Best Local Similarity 87.6% Pred. No. 1,66,04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

3 CTAAATATATCTAAAG 18
|||||
16 CTAAATATATCTAAAG 1

RESULT 38
AAA49413/c
10 AAA49413 standard; DNA; 19 BP.
XX
AAA49413;
25-SEP-2000 (first entry)
T7 terminator primer used for sequencing.
Hsp70; Hsp60; heat shock protein; immunogen; immunity; vaccination;
detection; Neisseria meningitidis; Aspergillus fumigatus;
Candida glabrata; primer; ss.
XX

OS Homo sapiens
XX XX
XX PN W0200129251 A2.
XX XX
XX PD 26 APR 2001.
XX XX
XX PE 18 OCT 2000; genome_w: 44174733.
XX XX
XX FR 18 OCT 1999; 93EB-0870216.
XX XX FR 03-JUN-2000; Z0004P-0870122.
XX XX FR 16 JUN 2000; Z0004bs-0211629.
XX XX
XX PA (HUGE) UNIV SENT.
PI Mississin L., Gallons T;
XX XX
XX WR17_2001-306341731
XX XX
XX PT Mutation analysis of NFI gene by treating EBV transformed lymphoblastoid cell lines formed with lymphocytes of patient with protein synthesis inhibition, and obtaining peptides by translating amplified RNA from cell line -
XX XX
XX PS Example 7, page 36, WO/97/02173 Published
XX XX
XX CC The DNA sequences following have been obtained from cDNA fragments A method for mutation analysis of the NFI gene involves isolating peripheral blood lymphocytes (PBL) of a patient, establishing Epstein Barr virus (EBV) transduced B lymphoblastoid cell line with selective drug or other agent containing a PBL by epithelialization (EPA) stimulation, leading the cell line to short-term culture with protein synthesis inhibitor and immediately extracting RNA from the cultures. The RNA is then amplified and rapidly fragmented. Mutagenesis analysis of transcribed/amplified and amplified fragments. Mutation analysis of NFI is used for detection of frame shift, missense and silent mutations. In various forms of the gene, this is useful in screening for NFI mutations in young children who are often oligoprenating. Efficacy of a model of a child can be identified by a screening process in which the modulation is monitored in vitro using cell systems in which the defective NFI gene is expressed. The sequences can be used to design drugs which modulate NFI activity, by using knowledge of the structure of the PPI proteins and specific defects of the various NFI mutant proteins. The method allows for reliable analysis of mutations that are difficult to detect due to instability of wrong-spliced transcripts

Sequence 32 BP; 2 A; 0 G; 9 C; 20 U; 1 Other;

Query Match 49.9%; Score 12.2; DB 22; Length 32;
Best Local Similarity 55.6%; Field No. 114904,
Matches 15; Conservative 1; Mismatches 4; Indels 0; Caps 0

CY A CAATACCTACGACAATA 27
||| ||||| ||||| |||
DB 27 CAAAGAAATACCAACAAACA 8

RESULT 12
AAH26287
ID AAH26287 of dbEST, ENA, CC PC
XX AAH26287;
XX AT
XX 02-OCT-2001 (first entry)
XX XX
XX DE IgG Transferring to receptor alpha chain FCB primer B).
XX XX
XX KW For reactivity, FCB, immunoglobulin J3, transferrin with, allusion, transgenic animal; ruminant; cattle; PCR primers ss.
XX XX
XX Rattus sp.

```

01 Mus sp.sapiens .
02 Homo sapiens .
XX XX W000197088-A1.
XX XX
XX XX 09-AUG-2001.
XX XX
XX XX 02 FEB 2000; JOURNAL OF BIOLOGY.
XX XX
XX XX 03 FEB 2000; JOURNAL OF BIOLOGY.
XX XX
XX XX (HAMM/) HAMMARSTROM L.
XX XX (RACS/) RAKSOVICS I.
XX XX
XX XX Hammarstrom L., Raksovcics I.;
XX XX MPI; 2001-493416/52.
XX XX
XX XX New DNA molecule encoding immunoglobulin G transporting human B-
XX XX receptor, FcγRI, useful for predicting presence of mice with enhanced
XX XX levels of immunoglobulins or proteins fused to immunoglobulin heavy
XX XX chains -
XX XX
XX XX Disclosures: Page 6, 4ff, English.
XX XX
XX XX The present sequence is that of degenerate primer H2, which is
XX XX based on a region of homology between rat, mouse and human γH1
XX XX transcripts in a region of homology between rat, mouse and human γH1
XX XX transcripts spanning the region of homology between rat, mouse and human
XX XX γH1 transcripts. It was used to amplify cDNA from spleen tissue of
XX XX mice infected with Friend B2 (see AM51292) in the presence of anti-FcγRI
XX XX antibody. The resulting cDNA fragments were ligated into the α1-
XX XX alpha-2 and alpha-3 extracellular domains of FcγRI was obtained.
XX XX Subsequent PCR amplification provided a full length
XX XX sequence (see AM51294). For amino acid sequence see AM51294. The
XX XX sequence relates to human major histocompatibility complex
XX XX class II gene polymorphisms, and may have been derived from a
XX XX cDNA library, and the protein encoded by them is also known as
XX XX a method of producing a polypeptide with enhanced levels of
XX XX immunoglobulins or proteins fused to immunoglobulin gamma chains or
XX XX their FcγRI interacting regions.
XX XX
XX XX Sequence 22 BP, 7 A, 6 C, 3 G, 3 T, 3 other;
XX XX
XX XX Query March 48 18 Score 13; DN 7% Length 207
XX XX Post local similarity for 48; Pseq No. 1.3e+04;
XX XX Matches 22, Conservation 2, Weight 100, Gap 10, Indel 10, Gap
XX XX
XX XX 6 AGTATATGTTAAATAAATA 24
XX XX |||||
XX XX 4 AGCATTACTAGTACCTACA 22
XX XX
XX XX RESULT 33
XX XX ID AI612188/c
XX XX AI612188 standard; DNA; 25 BP.
XX XX
XX XX AA162188;
XX XX
XX XX 16-OCT-2001 (first entry)
XX XX
XX XX Soybean 319013 region A1 DNA forward primer, SEQ ID NO: 819.
XX XX
XX XX Soybean 319013 region A1 DNA reverse primer, SEQ ID NO: 820.
XX XX
XX XX SCN resistance, rhg1, Rhg4, SCN resistant alleles plant breeding;
XX XX 24001 region G3; 319013 region A3; 515002 region G2; PCR primers;
XX XX Glycine max.
XX XX
XX XX W0009151627 A2.
XX XX
XX XX 13 JUL 1991.
XX XX
XX XX 24 JAN 2001; 2001W9 UNSECTED.
XX XX

```


|||||
11 CTTAGGCAATTAATCTAGC 28

RESULT 27

AAZ19837
ID AAZ19837 standard; DNA; 30 BP.

AC AAZ19837.

TT 06 DEC 1999 (first entry)

XX Bacteriophage T7 gene 10 terminator PCR primer #17.

XX Trehalose, biosynthesizes, inducible, stress tolerance, heat,

XX desiccation, osmotic shock, drought resistance, transgenic plant.

XX PCR, primer; ss.

XX Synthetic.

XX Bacteriophage T7.

XX W09946170 A2.

XX 09 MAR 1999; 99WO-EK01516.

XX 11 MAR 1998; 98US-0077665.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS EPFL/INMENSEN VEFM SEC MBH.

XX Label EG, Hefetz FB, Goff SA,

XX WFL 1999-561403/46.

XX New plant, 11-1999-561403/46.

XX protection against drought.

XX Example 11; Page 62; 10pp; English.

XX This sequence represents a bacteriophage T7 gene 10 terminator PCR

XX primer #17, used with primer #18 (AAZ19837) to construct a vector for

XX homologation in a bacterial host. A 1000 bp fragment of the

XX vector was then used to transform a host cell. The

XX (a D-glucopyranosyl) (1,4) a D-glucopyranosyl is a disaccharide

XX organisms such as bacteria, fungi and insects which acts as a

XX protectant against the deleterious effects of various stresses

XX such as heat, desiccation and osmotic shock. Trehalose biosynthesis

XX requires two enzymic activities: a trehalose 6-phosphate synthase

XX catalyzes the substitution of two glucose and glucose-6-phosphate to

XX phosphorylates trehalose-6-phosphate to trehalose. Previous

XX attempts have been made to express trehalose biosynthetic enzymes in

XX plants; however, certain deleterious effects appear to be associated

XX with expression of the trehalose synthase in the plant, particularly when

XX adverse effects include stunted growth, abnormal leaves and undeveloped

XX roots. The use of an inducible promoter prevents these effects

XX under the control of an inducible promoter can provide plants protected

XX against drought, high salinity, osmotic stress and temperature extremes.

XX They can also be used for increasing the storage properties of plants,

XX improving shelf-life of fruit and vegetables and preserving flowers.

XX They can also be used for stabilizing proteins expressed in transgenic

XX plants.

XX Sequence 10 REF: 11 A; 6 C; 7 G; 6 T; 0 other;

XX Query Match 48.93; Score 13.2; DB 20; Length 30;

XX Best Local Similarity 81.38; Find No. 1; 100.04;

XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

0Y 1 TCTGAGCAATTAATCTAGC 18
Db 9 TCTGAGCAATTAATCTAGC 26

RESULT 28

AAA29785
ID AAA29785 standard; DNA; 30 BP.

AC AAA29785.

XX 17 AUG 2000 (first entry)

XX Bacteriophage T7 gene 10 terminator PCR primer #17.

XX plant, transgenic, therapeutically active protein, fused to non-cy

XX vacuolar targeted vacuolar and immunoproteasome

XX allergy; autoimmune diseases; transplant rejection; etc. (first entry)

XX Bacteriophage T7.

XX W010020012 A2.

XX 05-OCT-1999; 99WO-EK07414.

XX 07-OCT-1998; 98US-0167362.

XX 07 OCT 1998; 98US-0168311.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS EPFL/INMENSEN VEFM SEC MBH.

XX Hefetz FB, Goff SA, Tullie AB, Gior-Wend MB.

XX WFL 2000-10908/28.

XX Novel transgenic plants expressing, therapeutically active proteins from

XX their plasmid genomes, useful for producing allergens for vaccines

XX Example 8; Page 47; 39pp; English.

XX The present invention describes plants (1) comprising a DNA molecule (1)

XX encoding a protein that is therapeutically active when expressed in a

XX host, in its plant genome. The transgenic plants are used to express

XX therapeutically active proteins, such as allergens, immunoproteasome

XX autoantigens. The therapeutically active proteins are used to treat or

XX prevent diseases, e.g. allergies, autoimmune diseases or transplant

XX rejection. The invention allows the production of large and numerous

XX supplies of protein based molecules. The plants are also used to express

XX large amounts of proteins in a cost-effective manner, and, as the

XX proteins are fused to plant proteins, they are to be used in vivo. The

XX present sequence represents a PCR primer which is used in an example

XX from the present invention.

XX Sequence 10 REF: 11 A; 6 C; 7 G; 6 T; 0 other;

XX Query Match 48.93; Score 13.2; DB 21; Length 30;

XX Best Local Similarity 81.38; Find No. 1; 100.04;

XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX Query Match 48.93; Score 13.2; DB 21; Length 30;

XX Best Local Similarity 81.38; Find No. 1; 100.04;

XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

XX Query Match 48.93; Score 13.2; DB 21; Length 30;

XX Best Local Similarity 81.38; Find No. 1; 100.04;

XX Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC within diagnostic fragment is selected and diagnostic fragments from
CC within the amplified and highly conserved regions in the fragment from
CC the positive panel which is less than 90 percent homologous to any member
CC of the negative panel are identified. Amplification primers to
CC diagnostic markers are designed and primer DNA of unknown bacteria are
CC amplified under suitable annealing temperatures, where at least 1
CC amplification product identifies a monotype of a member of *Listeria*
CC genus. The method uses known random amplified polymorphic DNA (RAPD)
CC application to identify fragments from the monotypes. The
CC methods are used to detect the presence of *Listeria* species in
CC food, human and animal body fluids or tissues, environmental media
CC or medical products and apparatus and are especially useful in the food
CC industry. The fragments shown in AAV37540 to AAV3764 are useful as
CC nucleic acid probes for identifying monotypes of the genus *Listeria*
CC detection not based on sequences derived from known species or associated
CC with known phenotypic characteristics, which was not previously
CC possible.

CC Sequence 26 BP; 10 A; 7 G; 4 C; 5 T; 0 other;

CC Query Match 48.9%; Score 13.2; DR 1%; Length 16;
CC Best Local Similarity 83.3%; Pred. No. 1.1e+04;

CC Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC 9 AATAGCTAATGCAACAAAT 26
CC ||||| |||||
CC 2 AATCCTTGAGGACAAAT 19

CC RESULT 24

CC AAV37562
CC ID AAV37562 standard; DNA; 26 BP;

CC AAV37562;

CC 09-SEP-1998 (first entry)

CC L. monocytogenes 1324 specific primer at 1515-26 (c233).

CC *Listeria monocytogenes* (EHEC) diagnostic fragment; pre marker;
CC random amplified polymorphic DNA application; food industry;

CC primer; ss.

CC Synthetic.

CC *Listeria monocytogenes*

CC W09820160 ALI

CC 14-MAY-1998.

CC 03-NOV-1997; 97MO-US10896.

CC 13-DEC-1996; 96US-0766439.

CC 08-NOV-1996; 96US-0745228.

CC (DDBP) DU PONT DE NEMOURS & CO E I.

CC Hazel JW, Jensen MA;

CC WPI; 1998-2666672.

CC Identifying *Listeria monocytogenes* or *Listeria* species using
CC random amplified polymorphic DNA application; food industry;

CC primer; DNA; diagnostic fragment; and primer;

CC (claim 17; Fig 3; 9pp) English.

CC Sequences shown in AAV37540 to AAV37577 are *Listeria* species specific
CC diagnostic primer sequences located at 1515 (c2341+2)-26-363,
CC 1515 (c2341+2)-27-363, 1515 (c2341+2)-27-363, 1515 (c2341+2)-27-363,
CC 1515 (c2341+2)-27-363 and 1515 (c2341+2)-27-363. The invention provides a
CC novel method of identifying *Listeria* monotypes or *Listeria* species
CC which comprises amplifying genomic DNA from positive and negative panels

CC of L. monotype strains and other *Listeria* strains representative with
CC primers (sequences shown in AAV37578 to AAV37593) located in the
CC the positive panel which is less than 90 percent homologous to any member
CC of the negative panel are identified. Amplification primers to
CC diagnostic markers are designed and primer DNA of unknown bacteria are
CC amplified under suitable annealing temperatures, where at least 1
CC amplification product identifies a monotype of a member of *Listeria*
CC genus. The method uses known random amplified polymorphic DNA (RAPD)
CC application to identify fragments from the monotypes. The
CC methods are used to detect the presence of *Listeria* species in
CC food, human and animal body fluids or tissues, environmental media
CC or medical products and apparatus and are especially useful in the food
CC industry. The fragments shown in AAV37540 to AAV3764 are useful as
CC nucleic acid probes for identifying monotypes of the genus *Listeria*
CC detection not based on sequences derived from known species or associated
CC with known phenotypic characteristics, which was not previously
CC possible.

CC Sequence 26 BP; 10 A; 7 G; 4 C; 5 T; 0 other;

CC Query Match 48.9%; Score 13.2; DR 1%; Length 16;
CC Best Local Similarity 83.3%; Pred. No. 1.1e+04;

CC Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CC 9 AATAGCTAATGCAACAAAT 26
CC ||||| |||||
CC 2 AATCCTTGAGGACAAAT 19

CC RESULT 24

CC AAX70663
CC ID AAX70663 standard; RNA; 27 BP;

CC AAX70663;

CC 29-JUL-1999 (first entry)

CC Human KDP VEGF receptor hamsterpad ribozyme #315.

CC Vascular endothelial growth factor receptor VEGF receptor; fig 1;
CC EHEC, KPI, *Hamamelis* 1:1 of 100, *Hamamelis* 1:1 of 100, *Hamamelis* 1:1 of 100;

CC tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular diseases;
CC fms-like tyrosine kinase 1; kinase insert domain containing receptor;

CC foetal liver kinase 1; ss.

CC Synthetic.

CC Homo sapiens.

CC W09715662 AC.

CC 01-MAY-1997.

CC 25-OCT-1996; 96MO-US17480.

CC 11-JAN-1996; 96US-0644040.

CC 26-OCT-1995; 95US-0005974.

CC (CHIEF) CHIEF CORP.

CC (SIBC) SIBCOWE PLASM INC.

CC Escobedo C, Moswipon C, Paves P, Stuchomb D;

CC WPI; 1997-259017/23.

CC Nucleic acid molecule containing VEGF receptor 1; gene expression of
CC RNA stability - useful for treating e.g. tumor angiogenesis,
CC psoriasis, rheumatoid arthritis, etc., in a human patient

BA (UNRE) INFO NEW JEPPEY
 XX
 P1 Madura K.
 XX
 DE WFL 1997 00322/04
 XX
 PT Nucleotide sequence as fusion of isolated proteins useful,
 PT respectively, for assessing the proliferative potential of malignant
 PT cells or to partly process complete
 XX
 PS Example 2: Page 29; 94FF, English.
 XX
 CC The present PCR primer was used to amplify regions 29 to 329 of DNA
 CC encoding the yeast PABC protein PABC containing a ubiquitin-like domain
 CC the ubiquitin-like domain was a major pathway for the proteasomal
 CC degradation of proteins, where the ubiquitin acts as a degradation
 CC signal. Proteins which bind the proteasome (a multisubunit complex)
 CC have ubiquitin-like (UBL) domain. When the UBL domains are fused to
 CC a reporter protein, they can be used to assess the proliferative
 CC potential and select drug resistance of malignant cells. The UBL
 CC domain also allows the identification of proteasomes for the isolation
 CC and characterization of novel substrates of the proteasome.
 XX
 SE Sequence 17 FF: 15 A, 7 G, 4 C, 4 T, 0 other.
 Query Match 51.4%, Score 13.42, EF 20, Length 32;
 Best Local Similarity 72.0%; Pred. No. 6, 1e-03;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 XX
 CY 1 TGTATGACCAATACCTACGACAA 25
 DB 7 TGTATGACCAAGACCAACTACGACA 31
 XX
 RESULT 14
 AA165664
 ID AA165664 standard, RNA, 24 BP.
 XX
 AC AA165664.
 XX
 DT 03-JAN-2002 (first entry)
 XX
 DE Primer for studying allelic polymorphic markers in the IBD1 region.
 XX
 KW Human; inflammatory bowel disease; protein; IBD1; IBDprox;
 KW intestinal inflammatory disease; apoptosis; NF-kappa B; cancer;
 KW inflammatory disease; immune disease; cryptosporidiosis; inflammation;
 KW homozygous; heterozygous; heterozygous; heterozygous; F5 primer; ss;
 XX
 OS Homo sapiens.
 XX
 FN FR2806739-A1.
 XX
 FD 28-SEP-2001.
 XX
 PF 27-MAR-2000; 2000R 0001832.
 XX
 FH 27-MAR-2000; 2000R 0001842.
 XX
 BA (UNRE) INFO NEW JEPPEY
 XX
 P1 Homo sapiens, Thymus G, Thymus M, Thymus S, Thymus M;
 XX
 DE WFL 1997 00322/04.
 XX
 PT New human nucleotide sequence associated with intestinal inflammatory
 PT disease, useful for diagnosis, prognosis and control of these diseases,
 PT also related proteins
 XX
 PS Example 4: Page 47; 97FF, French.
 XX
 SE The AA165664 28 were used to characterize allelic polymorphic
 SE markers in the IBD1 gene region. The IBD1 gene encodes an inflammatory

CC IBD1 disease; (IBD) polymorphic, which is associated with intestinal
 CC inflammatory disease. The specification also describes a polymorphic
 CC which is in proximity to IBD1, and is designated IBDprox. The IBD1
 CC gene is probably involved in regulation of apoptosis and activation
 CC of NF-kappa B. The IBD1 and IBDprox polymorphisms are useful as
 CC source of probes and primers, as source of antisense oligonucleotides,
 CC for recombinant production of polypeptides, and in screening for
 CC interactive compounds. The polypeptides are used to raise specific
 CC antibodies which useful for diagnostic detection or purification
 CC of IBD1 and IBDprox, to screen for specific binding agents, potential
 CC therapeutic agents. The IBD1 and IBDprox polymorphisms and
 CC polypeptides are useful for treatment and prevention of inflammatory
 CC and/or immune diseases of cancer, where associated with mutations in
 CC genes encoding IBD1 and IBDprox, especially with mutations in
 CC inflammatory gene IBD1 and IBDprox polymorphisms, IBD1 and IBDprox
 CC disease and IBD1 syndrome).
 XX
 SE Sequence 24 FF: 15 A, 7 G, 4 C, 4 T, 0 other.
 Query Match 51.4%, Score 13.42, EF 20, Length 32;
 Best Local Similarity 72.0%; Pred. No. 6, 1e-03;
 Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 XX
 CY 1 TGTATGACCAATACCTACGACAA 25
 DB 7 TGTATGACCAAGACCAACTACGACA 31
 XX
 RESULT 15
 AAX67421
 ID AAX67421 standard, RNA, 27 BP.
 XX
 AC AAX67421.
 XX
 DT 28-JUL-1999 (first entry)
 XX
 DE Human; IBD1; VEGF receptor; heterozygous; heterozygous; heterozygous;
 XX
 KW Vascular endothelial growth factor receptor; VEGF receptor; IBD1;
 KW IBD1; IBD1; heterozygous; heterozygous; heterozygous; heterozygous;
 KW heterozygous; heterozygous; heterozygous; heterozygous; heterozygous;
 KW heterozygous; heterozygous; heterozygous; heterozygous; heterozygous;
 KW heterozygous; heterozygous; heterozygous; heterozygous; heterozygous;
 XX
 OS Synthetic.
 XX
 FN Homo sapiens.
 XX
 FD 01-MAY-1997.
 XX
 PF 45-OCT-1996; 95W-US1480.
 XX
 FH 11-JAN-1996; 95W-US1480.
 XX
 FH 45-OCT-1996; 95W-US1480.
 XX
 BA (CHIR) CHIRON CORP.
 XX
 P1 (RIBO) KIBOZYME PHARM INC.
 XX
 DE Eschschol J, McGowan J, Ponce P, Stinchcomb D;
 XX
 DE WFL 1997 00322/04.
 XX
 PT Nucleic acid molecule containing VEGF receptor (R) for expression of
 PT RNA stability useful for treating e.g. tumor angiogenesis,
 PT psoriasis, rheumatoid arthritis, etc., in a human patient
 XX
 PS Claim 9, Page 51, 219FF; English.
 XX
 SE The present invention provides for a VEGF receptor which mediates
 SE the synthesis, expression and/or stability of a RNA encoding 1 or more
 SE regions of vascular endothelial growth factor (VEGF). A portion
 SE (preferably human) having a similar sequence with the level of the

